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NEWS 3	Oct 27	New Extraction Code PAX now available in Derwent Files
NEWS 4	Oct 27	SET ABBREVIATIONS and SET PLURALS extended in Derwent World Patents Index files
NEWS 5	Oct 27	Patent Assignee Code Dictionary now available in Derwent Patent Files
NEWS 6	Oct 27	Plasdoc Key Serials Dictionary and Echoing added to Derwent Subscriber Files WPIDS and WPIX
NEWS 7	Nov 29	Derwent announces further increase in updates for DWPI
NEWS 8	Dec 5	French Multi-Disciplinary Database PASCAL Now on STN
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=> s (protein disrupter) or protein-disrupter

L1 0 (PROTEIN DISRUPTER) OR PROTEIN-DISRUPTER

=> s developmental gene promoter

L2 0 DEVELOPMENTAL GENE PROMOTER

=> s aleurone

L3 5105 ALEURONE

=> s aleurone layer gene

L4 4 ALEURONE LAYER GENE

=> d l4 1-4 abs ibib

L4 ANSWER 1 OF 4 CAPLUS COPYRIGHT 2001 ACS
AB The effects of the maize genes, o2 and Mal, on the concns. of mineral nutrient cations and amino acid levels in mature maize (Zea mays L) kernels of various inbred lines were studied. Previously, the o2 gene has been used to improve the protein quality and increase the mineral nutrient content of kernels from some inbred lines. Genotypes possessing the Mal (multiple **aleurone layer**) **gene**, contain more than one row of aleurone cells in their kernels and this gene enhances the effect of the o2 gene on improving kernel protein quality. Incorporating these genes into the maize genome increased accumulation of several mineral nutrients (including Ca, Mg, Zn, Fe, Mn, Zn and Cu) in some of the exptl. lines studied. The physiol. basis for this increase of mineral nutrients in the kernels is discussed. The effect of the Mal gene on the kernel amino acid compn. and protein quality was also examd. Possibly, these genes could be used in combination in breeding programs to improve kernel quality and nutritional value of maize.

ACCESSION NUMBER: 1994:604290 CAPLUS
DOCUMENT NUMBER: 121:204290
TITLE: Improving the mineral reserves and protein quality of maize (Zea mays L.) kernels using unique genes
AUTHOR(S): Welch, R. M.; Smith, M. E.; Van Campen, D. R.; Schaefer, S. C.
CORPORATE SOURCE: U.S. Plant, Soil and Nutrition Laboratory, USDA, Ithaca, NY, USA
SOURCE: Dev. Plant Soil Sci. (1993), 54(Plant Nutrition), 235-8
CODEN: DVPSD8; ISSN: 0167-840X
DOCUMENT TYPE: Journal

LANGUAGE: English

L4 ANSWER 2 OF 4 CAPLUS COPYRIGHT 2001 ACS

AB The effects of the maize genes, o2 and Mal, on the concns. of mineral nutrient cations and amino acid levels in mature maize (Zea mays) kernels of various inbred lines were studied. Previously, the o2 gene has been used to improve the protein quality and increase the mineral nutrient content of kernels from some inbred lines. Genotypes possessing the Mal (multiple **aleurone layer**) **gene**, contain more than one row of aleurone cells in their kernels and this gene enhances the effect of the o2 gene on improving kernel protein quality. Incorporating these genes into the maize genome increased accumulation of several mineral nutrients (including Ca, Mg, Zn, Fe, Mn, K, and Cu) in some of the exptl. lines studied. The physiol. basis for this increase of mineral nutrients in the kernels is discussed. The effect of the Mal gene on the kernel amino acid compn. and protein quality was also examd. Possibly, these genes could be used in combination in breeding programs to improve kernel quality and nutritional value of maize.

ACCESSION NUMBER: 1994:212749 CAPLUS
DOCUMENT NUMBER: 120:212749
TITLE: Improving the mineral reserves and protein quality of maize (Zea mays L.) kernels using unique genes
AUTHOR(S): Welch, R. M.; Smith, M. E.; Van Campen, D. R.; Schaefer, S. C.
CORPORATE SOURCE: ARS U.S. Plant, Soil and Nutrit. Lab., USDA, Ithaca, NY, USA
SOURCE: Plant Soil (1993), 155-156, 215-18
CODEN: PLSOA2; ISSN: 0032-079X
DOCUMENT TYPE: Journal
LANGUAGE: English

L4 ANSWER 3 OF 4 BIOSIS COPYRIGHT 2001 BIOSIS

AB The effects of the maize genes, o-2 and Mal, on the concentrations of mineral nutrient cations and amino acid levels in mature maize (Zea mays L.) kernels of various inbred lines were studied. Previously, the o-2 gene has been used to improve the protein quality and increase the mineral nutrient content of kernels from some inbred lines. Genotypes possessing the Mal (multiple **aleurone layer**) **gene**, contain more than one row of aleurone cells in their kernels and this gene enhances the effect of the o-2 gene on improving kernel protein quality. Incorporating these genes into the maize genome increased accumulation of several mineral nutrients (including Ca, Mg, Zn, Fe, Mn, Zn and Cu) in some of the experimental lines studied. The physiological basis for this increase of mineral nutrients in the kernels is discussed. The effect of the Mal gene on the kernel amino acid composition and protein quality was also examined. Possibly, these genes could be used in combination in breeding programs to improve kernel quality and nutritional value of maize.

ACCESSION NUMBER: 1994:153049 BIOSIS
DOCUMENT NUMBER: PREV199497166049
TITLE: Improving the mineral reserves and protein quality of maize (Zea mays L.) kernels using unique genes.
AUTHOR(S): Welch, R. M. (1); Smith, M. E.; Van Campen, D. R.; Schaefer, S. C. (1)
CORPORATE SOURCE: (1) USDA-ARS U.S. Plant Soil Nutrition Lab., Ithaca, NY USA
SOURCE: Plant and Soil, (1993) Vol. 155-156, No. 0, pp. 215-218. ISSN: 0032-079X.
DOCUMENT TYPE: Article
LANGUAGE: English

L4 ANSWER 4 OF 4 [redacted]SIS COPYRIGHT 2001 BIOSIS

AB A disomic substitution line of 4E for 4D is named blue-grained wheat. It had its origin from the cross and backcrosses between Triticum L. and Agropyron elongatum (Host) Beauv (2n = 70) many years ago and was recently crossed again with common wheat, which resulted in a blue-grained monosomic wheat (for short, blue monosomic). This line has 40 wheat chromosomes and 1 Agropyron chromosome-4E carrying a blue **aleurone layer gene**. The selfed grains of blue monosomic could be grouped into 4 types: deep blue, medium blue, light blue and white, of which the chromosome numbers in the root-tip cells are 42, 41, 41 and 40, respectively. Many 4D-nullisomic plants of wheat were obtained from the progeny of blue monosomic. Some self-fertilized 4D-nullisomic lines were isolated by selection. They were used in the hybridization with Secale cereale L. and F1 plants with 27 chromosomes were obtained.

ACCESSION NUMBER: 1983:273407 BIOSIS
DOCUMENT NUMBER: BA76:30899
TITLE: BLUE GRAINED MONOSOMIC WHEAT 1.
AUTHOR(S): LI Z; MU S; JIANG L; ZHOU H; WU J; YU L
CORPORATE SOURCE: NORTHWEST INST. BOTANY, SHAANXI WUGONG.
SOURCE: ACTA GENET SIN, (1982 (RECD 1983)) 9 (6), 431-439.
CODEN: ICHPCG. ISSN: 0379-4172.
FILE SEGMENT: BA; OLD
LANGUAGE: Chinese

promoter which requires for activation, the presence of an exogenous chem. which may comprise an alc. Hydrolysis of the agriculturally acceptable ester results in the prodn. of the alc. One such example can be found in the fungal organism Aspergillus nidulans which expresses the enzyme alc. dehydrogenase encoded by the the gene **alcA** only when it is grown in the presence of various alcs. and ketones. The induction is relayed through a regulator protein encoded by the alcR gene and constitutively expressed. In the presence of inducer (alc.), the regulator protein activates the expression of the **alcA** gene and also stimulates expression of itself; conversely, the **alcA** gene and its product are not expressed in the absence of inducer. Thus, agriculturally acceptable esters are suitably translocated into the target plant in which the gene control system is in place and/or hydrolyzed either under environmental conditions or in the presence of a suitable catalytic moiety such as an enzyme or catalytic antibody, at rates which are appropriate to provide sufficient quantities of the activating alc. at the required time in the necessary parts of the plant. Appropriate selection of ester leads to a favored induction profile. Formulations of these esters are also described and claimed.

ACCESSION NUMBER: 2000:535295 CAPLUS
DOCUMENT NUMBER: 133:145902
TITLE: Ester/alcohol system for inducible gene expression system for use in plants
INVENTOR(S): Clarke, Eric Daniel; Chrystal, Ewan James Turner; Jepson, Ian; Paine, Jacqueline Ann Mary
PATENT ASSIGNEE(S): Zeneca Limited, UK
SOURCE: PCT Int. Appl., 37 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2000044917	A1	20000803	WO 1999-GB4348	19991222

W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

PRIORITY APPLN. INFO.: GB 1999-2234 19990201
OTHER SOURCE(S): MARPAT 133:145902
REFERENCE COUNT: 4
REFERENCE(S): (1) Gatz; NATURE BIOTECHNOLOGY 1998, V16, P140 CAPLUS
(2) Salter, M; PLANT JOURNAL 1998, V16(1), P127 CAPLUS
(3) Zeneca Ltd; WO 9706268 A 1997 CAPLUS
(4) Zeneca Ltd Gb; WO 9321334 A 1993 CAPLUS

L23 ANSWER 2 OF 84 CAPLUS COPYRIGHT 2001 ACS
AB The plasmid pALCA1SIFN contg. cDNA that encodes the human interferon .alpha.-2b was obtained from the ATCC (no. 531667). In this system the expression of the gene is under the control of an **alcA** **promoter**. **AlcA** p is a specific **promoter** for expression of different genes in Aspergillus filamentous. In this plasmid the coding region of IFN.alpha.-2b is preceded by the coding region of a synthetic signal peptide. For direct expression of the IFN.alpha.-2b gene

under the contr[redacted]of a T7/1 ac **promoter** of pET24[redacted]) expression vector, three s[redacted]cloning steps were carried out [redacted]ch resulted in the construction of 3 new plamids. PHA1, pHA2 and pHA4 in which the IFN.alpha.-2 gene is under the control of lacp, lacuv5p and T7 **promoter**, resp. Another plasmid, pHA3, was also constructed and is a modified version of pET24d(+). Provided there is a synthetic signal peptide preceding the coding region of IFN.alpha.2 gene, the protein can be seen in either system, as shown by western blotting, albeit with a different level of expression. The best product can be seen in the pHA4 plasmid with a T7p as judged by Dot and Western blotting.

ACCESSION NUMBER: 2000:101682 CAPLUS
DOCUMENT NUMBER: 133:115676
TITLE: Cloning and expression of a human interferon .alpha.2 gene in Escherichia coli
AUTHOR(S): Mehraein, F.; Akrami-Abarghoei, H.; Noori-Daloii, M. R.; Mostafaii, A.; Zadeh, M. Sadeghi
CORPORATE SOURCE: Pasteur Institute, Tehran, Iran
SOURCE: J. Sci., Islamic Repub. Iran (1999), 10(2), 85-92
CODEN: JSIIEN; ISSN: 1016-1104
PUBLISHER: National Center for Scientific Research
DOCUMENT TYPE: Journal
LANGUAGE: English
REFERENCE COUNT: 16
REFERENCE(S):
(1) Alton, K; In the Biology of the Interferon System 1983, P119 CAPLUS
(2) Bradford, M; Analytical Biochemistry 1976, V72, P248 CAPLUS
(3) Davanloo, P; Proc Natl Acad Sci USA 1984, V81, P2035 CAPLUS
(4) De Maeyer, E; Proc Natl Acad Sci USA 1982, V79, P4256 CAPLUS
(5) Edge, M; Biotech Genet Engineer, Rev 1984, V2, P215 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L23 ANSWER 3 OF 84 CAPLUS COPYRIGHT 2001 ACS
AB A general framework for a genetically structured model is presented. The framework allows description of the interactions in a system of regulatory and structural genes. The model assumes equil. kinetics for the binding of regulatory proteins to the **promoter** regions of the genes and includes the possible activation of proteins following their synthesis. The model is evaluated by simulating the **alcA**-expression (alc. dehydrogenase I) in Aspergillus nidulans which is an inducible system subject to glucose repression. The intracellular enzyme levels in strains with different regulatory mutations are simulated during various growth conditions. The model gives a good description of the exptl. data with changes in only a few parameter values which have a mechanistic interpretation.

ACCESSION NUMBER: 1999:808255 CAPLUS
DOCUMENT NUMBER: 132:107028
TITLE: Genetically structured modeling of protein production in filamentous fungi
AUTHOR(S): Agger, Teit; Nielsen, Jens
CORPORATE SOURCE: Center for Process Biotechnology, Department of Biotechnology, Technical University of Denmark, Lyngby, DK-2800, Den.
SOURCE: Biotechnol. Bioeng. (1999), 66(3), 164-170
CODEN: BIBIAU; ISSN: 0006-3592
PUBLISHER: John Wiley & Sons, Inc.
DOCUMENT TYPE: Journal
LANGUAGE: English
REFERENCE COUNT: 10
REFERENCE(S): (1) Agger, T; Biotechnol Bioeng 1998, V57(3), P321

CAPLUS
(2) Devit, M; Mol Biol Cell [illegible]7, V8, P1603 CAPLUS
(3) Endy, D; Biotechnol Bioeng 1997, V55, P375 CAPLUS
(4) Lee, S; Biotechnol Bioeng 1984, V26, P1372 CAPLUS
(5) Lee, S; Biotechnol Bioeng 1984, V26, P1383 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L23 ANSWER 4 OF 84 CAPLUS COPYRIGHT 2001 ACS

AB Methods of regulating the male or female sterility of plants using regulatory systems that can be induced by an external stimulus, e.g. chem., for plant breeding are described. Systems including mechanisms to restore fertility can also be used. Male-sterile, female-fertile and male-fertile, female sterile plants can be interplanted to allow cross-pollination and seed formation. The use of chem. regulated systems that can abort pollen or ovule development is discussed. Methods of inducing sporophytic and gametophytic sterility are described. Use of suitable expression constructs to regulate reporter gene expression in a no. of crop plant species is demonstrated.

ACCESSION NUMBER: 1999:549394 CAPLUS
DOCUMENT NUMBER: 131:155873
TITLE: Use of externally-regulated expression systems to control male and female fertility in plant breeding
INVENTOR(S): Knight, Mary Elizabeth; Jepson, Ian; Daly, Allan; Bayliss, Michael William
PATENT ASSIGNEE(S): Zeneca Limited, UK
SOURCE: PCT Int. Appl., 105 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9942598	A2	19990826	WO 1999-GB238	19990122
WO 9942598	A3	19991021		
W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
AU 9921790	A1	19990906	AU 1999-21790	19990122
BR 9908126	A	20001024	BR 1999-8126	19990122
EP 1054985	A2	20001129	EP 1999-901793	19990122
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				

PRIORITY APPLN. INFO.: GB 1998-3659 19980220
GB 1998-5669 19980317
WO 1999-GB238 19990122

L23 ANSWER 5 OF 84 CAPLUS COPYRIGHT 2001 ACS

AB The pollen-specific promoter of the C5 gene of Zea mays (ZmC5) that can be used for pollen-specific expression of foreign genes is described. Expression cassettes and expression systems as well as transformation methods, transformed plants including the promoter sequence of the invention are also claimed. The nucleic acid may be used inter alia in the prodn. of male sterile plants and/or hybrids as well as in the transformation of pollen. CDNAs for transcripts that were expressed in corn pollen, but not in shoots were identified by differential screening. A cDNA encoding a polygalacturonase-like protein was obtained and this

primary clone w[redacted]used to identify the gene in a[redacted]nomic library of B73 corn. Expressi[redacted] was limited strictly limited t[redacted]ature dehisced pollen and germinating pollen. Use of the promoter to drive expression of the barnase gene in pollen with the transgenic plants being male-sterile is demonstrated.

ACCESSION NUMBER: 1999:549383 CAPLUS
DOCUMENT NUMBER: 131:166254
TITLE: The pollen-specific promoter of the C5 gene of Zea mays
INVENTOR(S): Greenland, Andrew James; Rogers, Hilary Joan; Hussey, Patrick Joseph
PATENT ASSIGNEE(S): Zeneca Limited, UK
SOURCE: PCT Int. Appl., 34 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9942587	A1	19990826	WO 1999-GB232	19990122
W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
AU 9922876	A1	19990906	AU 1999-22876	19990122
BR 9907997	A	20001024	BR 1999-7997	19990122
EP 1054970	A1	20001129	EP 1999-902660	19990122
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
PRIORITY APPLN. INFO.:			GB 1998-3660	19980220
			GB 1998-3661	19980220
			WO 1999-GB232	19990122

REFERENCE COUNT: 7
REFERENCE(S):
(1) Albani, D; Plant Molecular Biology 1991, V16(4), P501 CAPLUS
(2) Greenland, A; WO 9704116 A 1997 CAPLUS
(3) ICI PLC; WO 9008830 A 1990 CAPLUS
(4) Lee, J; WO 9713401 A 1997 CAPLUS
(5) Scott, R; WO 9738116 A 1997 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L23 ANSWER 6 OF 84 CAPLUS COPYRIGHT 2001 ACS
AB It was found previously that the Aspergillus nidulans csmA gene encodes a novel protein which consists of an N-terminal myosin motor-like domain and a C-terminal chitin synthase domain. To clarify the roles of csmA in fungal morphogenesis, csmA null mutants were constructed. The growth rate of the mutant colonies was almost the same as that of the wild-type strain, but hyphal growth was severely inhibited when a chitin-binding reagent, Calcofluor white or Congo red, was added to the medium. Moreover, morphol. abnormalities in tip growth and septum formation were identified microscopically. Proliferation of intracellular new hyphae, called intrahyphal hyphae, which behaved as intrinsic hyphae, was the most striking phenotypic feature among them. These phenotypes were not suppressed when the only chitin synthase domain of csmA was expressed under the control of the **alcA promoter**, whereas they

were suppressed when the intact form of csmA was expressed. Therefore, it was concluded that the product of csmA (CsmA) has important roles in polarized cell wall synthesis and maintenance of cell wall integrity and that the myosin motor-like domain is indispensable for these functions.

ACCESSION NUMBER: 1999:398625 CAPLUS
DOCUMENT NUMBER: 131:167545
TITLE: Proliferation of intrahyphal hyphae caused by disruption of csmA, which encodes a class V chitin synthase with a myosin motor-like domain in Aspergillus nidulans
AUTHOR(S): Horiuchi, Hiroyuki; Fujiwara, Makoto; Yamashita, Shuichi; Ohta, Akinori; Takagi, Masamichi
CORPORATE SOURCE: Department of Biotechnology, The University of Tokyo, Tokyo, 113-8657, Japan
SOURCE: J. Bacteriol. (1999), 181(12), 3721-3729
CODEN: JOBAAY; ISSN: 0021-9193
PUBLISHER: American Society for Microbiology
DOCUMENT TYPE: Journal
LANGUAGE: English
REFERENCE COUNT: 35
REFERENCE(S):
(1) Aufauvre-Brown, A; Fungal Genet Biol 1997, V21, P141 CAPLUS
(2) Bartnicki-Garcia, S; Annu Rev Microbiol 1968, V22, P87 CAPLUS
(4) Borgia, P; Fungal Genet Biol 1996, V20, P193 CAPLUS
(5) Bowen, A; Proc Natl Acad Sci USA 1992, V89, P519 CAPLUS
(6) Bulawa, C; Annu Rev Microbiol 1993, V47, P505 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L23 ANSWER 7 OF 84 CAPLUS COPYRIGHT 2001 ACS
AB The invention describes a method of increasing the yield of a plant by selectively controlling the expression of DNA sequences coding for proteins involved in the transport, metab. and uptake of sucrose. The method allows for the controlled alteration of sucrose levels in the plant to produce a desired change in flowering, plant wt., and/or height at the appropriate stage in plant growth whereby any effects deleterious to the plant are avoided and the overall yield of the plant is increased. In a preferred embodiment, the invention involves increasing transportation of fixed carbon from photosynthetically active source tissue to photosynthetically inactive sink tissue by transforming a plant with a DNA construct comprising one or more DNA sequences coding for a protein involved in sucrose sensing, transport, metab., and/or uptake operably linked to an **alcA**/alcR gene switch **promoter** system. The level, time and spatial location of expression of said DNA sequence(s) are controlled by application of an external chem. inducer, resulting in increased plant yield.

ACCESSION NUMBER: 1999:388312 CAPLUS
DOCUMENT NUMBER: 131:40548
TITLE: Method of increasing plant yield by selectively controlling the expression of DNA sequences coding for proteins involved in the transport, metab. and uptake of sucrose
INVENTOR(S): Jepson, Ian; Chu, Chengcai; Qu, Nan; Sonnewald, Uwe
PATENT ASSIGNEE(S): Zeneca Limited, UK
SOURCE: PCT Int. Appl., 43 pp.
CODEN: PIXXD2

DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9929881	A1	19990617	WO 1998-GB3687	19981210
W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
AU 9914961	A1	19990628	AU 1999-14961	19981210
EP 1036184	A1	20000920	EP 1998-959028	19981210
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				

PRIORITY APPLN. INFO.: EP 1997-121829 19971211
WO 1998-GB3687 19981210

REFERENCE COUNT: 5
REFERENCE(S):
(1) Caddick, M; WO 9321334 A 1993 CAPLUS
(2) Caddick, M; Nature Biotechnology 1998, V16, P177 CAPLUS
(3) Cambridge Advanced Tech; EP 0438904 A 1991 CAPLUS
(4) Inst Genbiologische Forschung; EP 0442592 A 1991
(5) Riesmeier, J; WO 9707221 A 1997 CAPLUS

L23 ANSWER 8 OF 84 CAPLUS COPYRIGHT 2001 ACS
AB The invention provides a means of controlling sprouting in vegetative storage organs, such as potato tubers, such that sprouting may be turned off and on without any undesirable side effects. The method involves the use of target and organ specific promoters to control expression of DNA sequences to inhibit sprouting. Sprouting is restored by switching on expression of DNA sequences using inducible promoter regions where sprouting may be controlled by, for example, application of an external chem. stimulus.
ACCESSION NUMBER: 1999:113828 CAPLUS
DOCUMENT NUMBER: 130:192735
TITLE: Genetic method for controlling sprouting in potato tubers
INVENTOR(S): Jepson, Ian; Ebneth, Marcus; Sonnewald, Uwe
PATENT ASSIGNEE(S): Zeneca Limited, UK
SOURCE: PCT Int. Appl., 89 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9906578	A2	19990211	WO 1998-GB2023	19980710
WO 9906578	A3	19990422		
W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				

AU 9882341	A1	19990222	AU 1998-82[redacted]	19980710
EP 1017830	A1	20000712	EP 1998-93[redacted]2	19980710
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
BR 9811493	A	20000919	BR 1998-11493	19980710
PRIORITY APPLN. INFO.:			EP 1997-113118	19970730
			WO 1998-GB2023	19980710

L23 ANSWER 9 OF 84 CAPLUS COPYRIGHT 2001 ACS

AB We describe a chem. induced gene control mechanism for plants based on the ALCR transcription factor and **alcA promoter** of Aspergillus nidulans, which we have called the alc system. Ethanol, the chem. inducer, is not toxic at levels required for induction, and can be applied to the plants by spraying, root drenching and addn. to liq. growth media. The alc system is very sensitive to ethanol and the induction is rapid; 0.01% (1.7 mM) ethanol in liq. growth media initiates chloramphenicol acetyl transferase (CAT) reporter gene expression within 4 h, with maximal expression occurring after 4 days. In the complete absence of ethanol, there is no detectable expression of CAT, nor do we observe induction in plants subjected to wound, cold or drought stress, or following treatment with either salicylic acid or Me jasmonate. However, extreme anoxia resulting in elevated levels of alc. dehydrogenase activity in both roots and leaves gave substantial induction of CAT in leaves but not in roots. We believe that the alc system will have broad utility in the exogenous control of plant gene expression in pure science and that it also has considerable potential in agriculture.

ACCESSION NUMBER:	1998:717437 CAPLUS
DOCUMENT NUMBER:	130:105798
TITLE:	Characterization of the ethanol-inducible alc gene expression system for transgenic plants
AUTHOR(S):	Salter, Michael G.; Paine, Jacqueline A.; Riddell, Kay V.; Jepson, Ian; Greenland, Andrew J.; Caddick, Mark X.; Tomsett, A. Brian
CORPORATE SOURCE:	School of Biological Sciences, Donnan Laboratories, The University of Liverpool, Liverpool, L69 7ZD, UK
SOURCE:	Plant J. (1998), 16(1), 127-132 CODEN: PLJUED; ISSN: 0960-7412
PUBLISHER:	Blackwell Science Ltd.
DOCUMENT TYPE:	Journal
LANGUAGE:	English
REFERENCE COUNT:	14
REFERENCE(S):	(2) Bevan, M; Nucl Acids Res 1984, V12, P8711 CAPLUS (4) Caddick, M; Nature Biotech 1998, V16, P177 CAPLUS (5) Felenbok, B; Gene 1988, V73, P385 CAPLUS (7) Gatz, C; Annu Rev Plant Physiol Plant Mol Biol 1997, V48, P89 CAPLUS (9) Neumann, J; Biotechniques 1987, V5, P444 CAPLUS ALL CITATIONS AVAILABLE IN THE RE FORMAT

L23 ANSWER 10 OF 84 CAPLUS COPYRIGHT 2001 ACS

AB We have investigated the minimal requirements of the tail region for myosin I function in vivo using the filamentous fungus Aspergillus nidulans. The CL3 strain (McGoldrick, C. A., et al., 1995) was transformed with a variety of myoA constructs contg. mutations in the IQ, TH-1-like, SH3, and proline-rich domains by frameshift or in-frame deletions of the tail domains. The resulting strains contained wild type myoA driven by the **alcA promoter** and a mutant myoA driven by its endogenous **promoter**. This strategy allowed for

selective expre[redacted]on of the wild type and/or muta[redacted] form of MYOA by the choice of growth [redacted]edium. Proper septation and hy[redacted]al branching were dependent on the interaction of the IQ motifs with calmodulin, as well as, the presence of its proline-rich domain. Addnl., a single proline-rich motif was sufficient for nearly wild type MYOA function. Most surprisingly, the SH3 domain was not essential for MYOA function. These studies expand our previous knowledge of the function of MYOA to include roles in hyphal morphogenesis, septal wall formation, and cell polarity, laying the groundwork for more detailed investigations on the function of the various tail domains in MYOA.

ACCESSION NUMBER: 1998:672128 CAPLUS
DOCUMENT NUMBER: 130:12244
TITLE: Structural requirements for in vivo myosin I function in Aspergillus nidulans
AUTHOR(S): Osherov, Nir; Yamashita, Roxanne A.; Chung, Yun-Shin; May, Gregory S.
CORPORATE SOURCE: Department of Cell Biology, Baylor College of Medicine, Houston, TX, 77030, USA
SOURCE: J. Biol. Chem. (1998), 273(41), 27017-27025
CODEN: JBCHA3; ISSN: 0021-9258
PUBLISHER: American Society for Biochemistry and Molecular Biology
DOCUMENT TYPE: Journal
LANGUAGE: English
REFERENCE COUNT: 27
REFERENCE(S): (1) Baines, I; J Cell Biol 1995, V130, P591 CAPLUS
(2) Brown, S; Curr Opin Cell Biol 1997, V9, P44 CAPLUS
(3) Durfee, T; Genes Dev 1993, V7, P555 CAPLUS
(4) Feinberg, A; Anal Biochem 1983, V132, P6 CAPLUS
(5) Feng, S; Science 1994, V266, P1241 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

=> d l24 1-10 abs ibib

L24 ANSWER 1 OF 36 CAPLUS COPYRIGHT 2001 ACS
AB An agriculturally acceptable hydrolyzable ester is used in the control of expression of a plant gene, said control being effected by an inducible **promoter** which requires for activation, the presence of an exogenous chem. which may comprise an alc. Hydrolysis of the agriculturally acceptable ester results in the prodn. of the alc. One such example can be found in the fungal organism Aspergillus nidulans which expresses the enzyme alc. dehydrogenase encoded by the the gene alcA only when it is grown in the presence of various alcs. and ketones. The induction is relayed through a regulator protein encoded by the **alcR** gene and constitutively expressed. In the presence of inducer (alc.), the regulator protein activates the expression of the alcA gene and also stimulates expression of itself; conversely, the alcA gene and its product are not expressed in the absence of inducer. Thus, agriculturally acceptable esters are suitably translocated into the target plant in which the gene control system is in place and/or hydrolyzed either under environmental conditions or in the presence of a suitable catalytic moiety such as an enzyme or catalytic antibody, at rates which are appropriate to provide sufficient quantities of the activating alc. at the required time in the necessary parts of the plant. Appropriate selection of ester leads to a favored induction profile. Formulations of these esters are also described and claimed.
ACCESSION NUMBER: 2000:535295 CAPLUS

DOCUMENT NUMBER: 133:145902
TITLE: Ester/alcohol system for inducible gene expression system for use in plants
INVENTOR(S): Clarke, Eric Daniel; Chrystal, Ewan James Turner; Jepson, Ian; Paine, Jacqueline Ann Mary
PATENT ASSIGNEE(S): Zeneca Limited, UK
SOURCE: PCT Int. Appl., 37 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2000044917	A1	20000803	WO 1999-GB4348	19991222

W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

PRIORITY APPLN. INFO.: GB 1999-2234 19990201
OTHER SOURCE(S): MARPAT 133:145902
REFERENCE COUNT: 4
REFERENCE(S): (1) Gatz; NATURE BIOTECHNOLOGY 1998, V16, P140 CAPLUS
(2) Salter, M; PLANT JOURNAL 1998, V16(1), P127 CAPLUS
(3) Zeneca Ltd; WO 9706268 A 1997 CAPLUS
(4) Zeneca Ltd Gb; WO 9321334 A 1993 CAPLUS

L24 ANSWER 2 OF 36 CAPLUS COPYRIGHT 2001 ACS
AB The **alcR** gene of Aspergillus nidulans, which encodes the specific transactivator of the ethanol utilization pathway, is pos. autoregulated and carbon catabolite repressed. Regulation by these two circuits occurs at the transcriptional level via the binding of the two regulators, **AlcR** and CreA, to their cognate targets resp. We demonstrate here that out of two clustered putative **AlcR** repeated consensus sequences, only the palindromic target is functional in vivo. Hence, it is solely responsible for the **alcR** pos. autogenous activation loop. Transcript mapping of the **alcR** gene showed that transcription initiation can occur at 553 bp and at or near 86 bp upstream of the start codon. These transcription start sites yield a transcript of 3.0 kb, which appears only under induced growth conditions, and of 2.6 kb, which is present under both induced and non-induced growth conditions resp. Nine CreA consensus sites are present in the **alcR promoter** but only two pairs of two sites are functional in vivo. One of them is located in close proximity to the **AlcR** functional target. Within this pair, both sites are necessary to mediate a partial repression of **alcR** transcription. Disruption of either site results in an overexpression of **alcR** due to the absence of direct competition between **AlcR** and CreA for the same DNA region. The second functional pair of CreA sites is located between the two transcription initiation sites. Disruption of either of the two sites results in a totally derepressed **alcR** transcription, showing that they work as a pair constituting the more efficient repression mechanism. Thus, CreA acts by two different mechanisms: by competing with **AlcR** for the same DNA region and by an efficient direct repression. The latter mechanism presumably interferes with the general transcriptional machinery.

ACCESSION NUMBER: 2000:298495 CAPLUS
DOCUMENT NUMBER: 133:203750
TITLE: In vivo studies of upstream regulatory cis-acting elements of the alcR gene encoding the transactivator of the ethanol regulon in Aspergillus nidulans
AUTHOR(S): Mathieu, Martine; Fillinger, Sabine; Felenbok, B.
CORPORATE SOURCE: Institut de Genetique et Microbiologie, Unite Mixte de Recherche CNRS no. 8621, Universite Paris-Sud, Centre Universitaire d'Orsay, Orsay, F-91405, Fr.
SOURCE: Mol. Microbiol. (2000), 36(1), 123-131
CODEN: MOMIEE; ISSN: 0950-382X
PUBLISHER: Blackwell Science Ltd.
DOCUMENT TYPE: Journal
LANGUAGE: English
REFERENCE COUNT: 39
REFERENCE(S):
(2) Ascone, I; Biochim Biophys Acta 1997, V1343, P211 CAPLUS
(3) Bailey, C; Eur J Biochem 1975, V51, P573 CAPLUS
(5) Cerdan, R; FEBS Microbiol Lett 1997, V408, P235 CAPLUS
(8) Dowzer, C; Mol Cell Biol 1991, V11, P5701 CAPLUS
(9) Felenbok, B; Gene 1988, V73, P385 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L24 ANSWER 3 OF 36 CAPLUS COPYRIGHT 2001 ACS
AB The invention relates to the isolation and characterization of novel expansin gene sequences from heterologous and homologous tree species and re-introducing such novel genes into trees so as to alter expansin levels.

Six novel genes from Eucalyptus grandis are identified. Eucalyptus is also transformed using the cucumber Ex29 sequence (GenBank, Accession No. U30382). A change in the plant height and internode length is obsd. compared with control plants.

ACCESSION NUMBER: 2000:161454 CAPLUS
DOCUMENT NUMBER: 132:204054
TITLE: Transformation of tree fibers with expansin genes from Eucalyptus or cucumber
INVENTOR(S): Burrell, Michael Meyrick; Cambridge, Amanda; Maunders, Martin Jack; Mcqueen-mason, Simon
PATENT ASSIGNEE(S): Advanced Technologies (Cambridge) Limited, UK
SOURCE: PCT Int. Appl., 49 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2000012715	A1	20000309	WO 1999-GB2746	19990818
W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KP, KR, KZ, LC, LK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
AU 9954361	A1	20000321	AU 1999-54361	19990818
PRIORITY APPLN. INFO.:			GB 1998-18808	19980829
			WO 1999-GB2746	19990818

REFERENCE COUNT: 4

REFERENCE(S): (1) Cambridge, A; ANNUAL MEETING OF THE SOCIETY FOR EXPERIMENTAL BIOLOGY 1999
(2) Cambridge, A; JOURNAL OF EXPERIMENTAL BOTANY V50(SUPPL), P36
(3) Eunwoon, N; RESEARCH REPORT OF THE FOREST GENETICS 1995, 31, P153
(4) Maunders, M; PROCEEDINGS OF THE SECOND INTERNATIONAL WOOD BIOTECHNOLOGY SYMPOSIUM 1999, P136

L24 ANSWER 4 OF 36 CAPLUS COPYRIGHT 2001 ACS

AB The invention describes a method of increasing the yield of a plant by selectively controlling the expression of DNA sequences coding for proteins involved in the transport, metab. and uptake of sucrose. The method allows for the controlled alteration of sucrose levels in the plant to produce a desired change in flowering, plant wt., and/or height at the appropriate stage in plant growth whereby any effects deleterious to the plant are avoided and the overall yield of the plant is increased. In a preferred embodiment, the invention involves increasing transportation of fixed carbon from photosynthetically active source tissue to photosynthetically inactive sink tissue by transforming a plant with a DNA construct comprising one or more DNA sequences coding for a protein involved in sucrose sensing, transport, metab., and/or uptake operably linked to an alcA/**alcR** gene switch **promoter** system. The level, time and spatial location of expression of said DNA sequence(s) are controlled by application of an external chem. inducer, resulting in increased plant yield.

ACCESSION NUMBER: 1999:388312 CAPLUS
DOCUMENT NUMBER: 131:40548
TITLE: Method of increasing plant yield by selectively controlling the expression of DNA sequences coding for proteins involved in the transport, metab. and uptake of sucrose
INVENTOR(S): Jepson, Ian; Chu, Chengcai; Qu, Nan; Sonnewald, Uwe
PATENT ASSIGNEE(S): Zeneca Limited, UK
SOURCE: PCT Int. Appl., 43 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9929881	A1	19990617	WO 1998-GB3687	19981210
W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
AU 9914961	A1	19990628	AU 1999-14961	19981210
EP 1036184	A1	20000920	EP 1998-959028	19981210
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
PRIORITY APPLN. INFO.:			EP 1997-121829	19971211
			WO 1998-GB3687	19981210

REFERENCE COUNT: 5
REFERENCE(S):
(1) Caddick, M; WO 9321334 A [illegible]3 CAPLUS
(2) Caddick, M; Nature Biotechnology 1998, V16, P177 CAPLUS
(3) Cambridge Advanced Tech; EP 0438904 A 1991 CAPLUS
(4) Inst Genbiologische Forschung; EP 0442592 A 1991
(5) Riesmeier, J; WO 9707221 A 1997 CAPLUS

L24 ANSWER 5 OF 36 CAPLUS COPYRIGHT 2001 ACS

AB In Aspergillus nidulans, the transcriptional activator AlcR mediates specific induction of a no. of alc genes. The AlcR DNA-binding domain is a zinc binuclear cluster that differs from the other members of the Zn2Cys6 family in several respects. Of these, the most remarkable is its ability to bind in vitro as a monomer to single sites, whereas only repeated sites (direct or inverted) are necessary and functional in vivo. Deletion of the first five amino acids (following the N-terminal methionine) upstream of the AlcR zinc cluster or mutation of a single residue, Arg-6, impairs the AlcR in vitro binding mainly to sym. sites. In vivo, the same mutations result in the inability of A. nidulans to grow on ethanol. The alc- phenotype results from a drastic decrease in activation of its own transcription and, in addn., that of the two structural genes, alcA and aldA, required for ethanol oxidn. This defect seems to be correlated to the inability of the Arg-6 AlcR mutant protein to bind to AlcR palindrome targets, which are essential in the three alc promoters. AlcR shows a unique pattern of binding and of transactivation among the Zn2Cys6 family.

ACCESSION NUMBER: 1999:159066 CAPLUS
DOCUMENT NUMBER: 130:333636
TITLE: A single amino acid, outside the AlcR zinc binuclear cluster, is involved in DNA binding and in transcriptional regulation of the alc genes in Aspergillus nidulans
AUTHOR(S): Nikolaev, Igor; Cochet, Marie-Francoise; Lenouvel, Francois; Felenbok, Beatrice
CORPORATE SOURCE: Institut de Genetique et Microbiologie, Unite de Recherche Associee au CNRS no. 2225, Universite Paris-Sud, Centre Universitaire d'Orsay, Orsay, F-91405, Fr.
SOURCE: Mol. Microbiol. (1999), 31(4), 1115-1124
CODEN: MOMIEE; ISSN: 0950-382X
PUBLISHER: Blackwell Science Ltd.
DOCUMENT TYPE: Journal
LANGUAGE: English
REFERENCE COUNT: 38
REFERENCE(S):
(1) Ascone, I; Biochim Biophys Acta 1997, V1343, P211 CAPLUS
(2) Camier, S; Mol Cell Biol 1992, V12, P5758 CAPLUS
(3) Cerdan, R; FEBS Lett 1997, V408, P235 CAPLUS
(5) Chiu, W; Curr Biol 1996, V6, P325 CAPLUS
(7) Felenbok, B; Gene 1988, V73, P385 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L24 ANSWER 6 OF 36 CAPLUS COPYRIGHT 2001 ACS

AB The invention provides a means of controlling sprouting in vegetative storage organs, such as potato tubers, such that sprouting may be turned off and on without any undesirable side effects. The method involves the use of target and organ specific promoters to control expression of DNA sequences to inhibit sprouting. Sprouting is restored by switching on expression of DNA sequences using inducible promoter regions where sprouting may be controlled by, for example, application of an external chem. stimulus.

ACCESSION NUMBER: 1999:113828 CAPLUS
DOCUMENT NUMBER: 130:192735
TITLE: Genetic method for controlling sprouting in potato

tubers
INVENTOR(S): Jepson, Ian; Ebneth, Marcus; [redacted]newald, Uwe
PATENT ASSIGNEE(S): Zeneca Limited, UK
SOURCE: PCT Int. Appl., 89 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9906578	A2	19990211	WO 1998-GB2023	19980710
WO 9906578	A3	19990422		
W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
AU 9882341	A1	19990222	AU 1998-82341	19980710
EP 1017830	A1	20000712	EP 1998-932412	19980710
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
BR 9811493	A	20000919	BR 1998-11493	19980710
PRIORITY APPLN. INFO.:			EP 1997-113118	19970730
			WO 1998-GB2023	19980710

L24 ANSWER 7 OF 36 CAPLUS COPYRIGHT 2001 ACS
AB We describe a chem. induced gene control mechanism for plants based on the **ALCR** transcription factor and alcA **promoter** of Aspergillus nidulans, which we have called the alc system. Ethanol, the chem. inducer, is not toxic at levels required for induction, and can be applied to the plants by spraying, root drenching and addn. to liq. growth media. The alc system is very sensitive to ethanol and the induction is rapid; 0.01% (1.7 mM) ethanol in liq. growth media initiates chloramphenicol acetyl transferase (CAT) reporter gene expression within 4 h, with maximal expression occurring after 4 days. In the complete absence of ethanol, there is no detectable expression of CAT, nor do we observe induction in plants subjected to wound, cold or drought stress, or following treatment with either salicylic acid or Me jasmonate. However, extreme anoxia resulting in elevated levels of alc. dehydrogenase activity in both roots and leaves gave substantial induction of CAT in leaves but not in roots. We believe that the alc system will have broad utility in the exogenous control of plant gene expression in pure science and that it also has considerable potential in agriculture.
ACCESSION NUMBER: 1998:717437 CAPLUS
DOCUMENT NUMBER: 130:105798
TITLE: Characterization of the ethanol-inducible alc gene expression system for transgenic plants
AUTHOR(S): Salter, Michael G.; Paine, Jacqueline A.; Riddell, Kay V.; Jepson, Ian; Greenland, Andrew J.; Caddick, Mark X.; Tomsett, A. Brian
CORPORATE SOURCE: School of Biological Sciences, Donnan Laboratories, The University of Liverpool, Liverpool, L69 7ZD, UK
SOURCE: Plant J. (1998), 16(1), 127-132

CODEN: PLJUED; ISSN: 0960-741[redacted]
PUBLISHER: Blackwell Science Ltd.
DOCUMENT TYPE: Journal
LANGUAGE: English
REFERENCE COUNT: 14
REFERENCE(S):
(2) Bevan, M; Nucl Acids Res 1984, V12, P8711 CAPLUS
(4) Caddick, M; Nature Biotech 1998, V16, P177 CAPLUS
(5) Felenbok, B; Gene 1988, V73, P385 CAPLUS
(7) Gatz, C; Annu Rev Plant Physiol Plant Mol Biol 1997, V48, P89 CAPLUS
(9) Neumann, J; Biotechniques 1987, V5, P444 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L24 ANSWER 8 OF 36 CAPLUS COPYRIGHT 2001 ACS
AB Carbon catabolite repression is mediated in Aspergillus nidulans by the neg. acting protein CreA. The CreA repressor plays a major role in the control of the expression of the alc regulon, encoding proteins required for the ethanol utilization pathway. It represses directly, at the transcriptional level, the specific transacting gene **alcR**, the two structural genes alcA and aldA, and other alc genes in all physiol. growth conditions. Among the seven putative CreA sites identified in the alcA **promoter** region, we have detd. the CreA functional targets in **AlcR** constitutive and derepressed genetic backgrounds. Two different divergent CreA sites, of which one overlaps a functional **AlcR** inverted repeat site, are largely responsible for alcA repression. Totally derepressed alcA expression is achieved when these two CreA sites are disrupted in addn. to another single site, which overlaps the functional palindromic induction target. The fact that derepression is always assocd. with alcA overexpression is consistent with a competition model between **AlcR** and CreA for their cognate targets in the same region of the alcA promotor. Our results also indicate that the CreA repressor is necessary and sufficient for the total repression of the alcA gene.
ACCESSION NUMBER: 1998:212644 CAPLUS
DOCUMENT NUMBER: 128:317932
TITLE: The CreA repressor is the sole DNA-binding protein responsible for carbon catabolite repression of the alcA gene in Aspergillus nidulans via its binding to a couple of specific sites
AUTHOR(S): Panozzo, Cristina; Cornillot, Emmanuel; Felenbok, Beatrice
CORPORATE SOURCE: Institut de Genetique et Microbiologie, Universite Paris-Sud, URA CNRS D 2225, Centre Universitaire d'Orsay, Orsay, F-91405, Fr.
SOURCE: J. Biol. Chem. (1998), 273(11), 6367-6372
CODEN: JBCHA3; ISSN: 0021-9258
PUBLISHER: American Society for Biochemistry and Molecular Biology
DOCUMENT TYPE: Journal
LANGUAGE: English

L24 ANSWER 9 OF 36 CAPLUS COPYRIGHT 2001 ACS
AB **AlcR** is the transactivator mediating transcriptional induction of the alc gene cluster in Aspergillus nidulans. The **AlcR** DNA-binding domain consists of a zinc binuclear cluster different from the other members of the Zn2Cys6 family by several features. In particular, it is able to bind to sym. and asym. sites with the same affinity, with both sites being functional in A. nidulans. Here, the authors show that unlike the other proteins of the Zn2Cys6 binuclear cluster family, **AlcR** binds most probably as a monomer to its cognate targets. Two mols. of the **AlcR** protein can simultaneously bind in

noncooperative [redacted]er to inverted repeats. The [redacted]sensus core has been detd. precisely [redacted]-CCGCN-3'), and the **AlcR**-bindi[redacted] site in the aldA **promoter** has been localized. The sequence downstream of the zinc cluster is necessary for high affinity binding. Furthermore, these data show that the use of the carrier protein glutathione S-transferase in **AlcR** binding expts. introduces an important bias in the recognition of DNA sites due to its tertiary dimeric structure.

ACCESSION NUMBER: 1997:397502 CAPLUS
DOCUMENT NUMBER: 127:105796
TITLE: In vitro recognition of specific DNA targets by AlcR, a zinc binuclear cluster activator different from the other proteins of this class
AUTHOR(S): Lenouvel, Francois; Nikolaev, Igor; Felenbok, Beatrice
CORPORATE SOURCE: Institut de Genetique et Microbiologie, URA CNRS D 2225, Universite Paris-Sud, Orsay, F-91405, Fr.
SOURCE: J. Biol. Chem. (1997), 272(24), 15521-15526
CODEN: JBCHA3; ISSN: 0021-9258
PUBLISHER: American Society for Biochemistry and Molecular Biology
DOCUMENT TYPE: Journal
LANGUAGE: English

L24 ANSWER 10 OF 36 CAPLUS COPYRIGHT 2001 ACS
AB Disclosed is a chem. inducible expression cassette for expression of a herbicide resistance gene in transgenic plants, using the alcA/alcR switch derived from Aspergillus nidulans. The DNA constructs are capable of conferring on a plant inducible resistance to a herbicide. The invention relates in particular to inducible resistance to the herbicide N-phosphonomethyl glycine (glyphosate) and its salts. Inducible expression of glyphosate oxidoreductase (GOX) and 5-enolpyruvyl-3-phosphoshikimic acid synthase (EPSPS) in transgenic plants was shown.

ACCESSION NUMBER: 1997:234349 CAPLUS
DOCUMENT NUMBER: 126:221460
TITLE: Chemically inducible plant expression vectors encoding herbicide resistance in transgenic plants
INVENTOR(S): Jepson, Ian
PATENT ASSIGNEE(S): Zeneca Limited, UK; Jepson, Ian
SOURCE: PCT Int. Appl., 57 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9706269	A1	19970220	WO 1996-GB1883	19960802
W: AL, AM, AT, AU, AZ, BB, BG, BR, BY, CA, CH, CN, CZ, DE, DK, EE, ES, FI, GB, GE, HU, IL, IS, JP, KE, KG, KP, KR, KZ, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, TJ, TM, TR, TT, UA, UG, US, UZ, VN, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: KE, LS, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA				
CA 2224732	AA	19970220	CA 1996-2224732	19960802
AU 9666278	A1	19970305	AU 1996-66278	19960802
AU 711653	B2	19991021		
EP 843730	A1	19980527	EP 1996-925925	19960802
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
CN 1197483	A	19981028	CN 1996-197232	19960802

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     BR 9609886          [redacted]    19990525        BR 1996-988[redacted]    19960802
     JP 11510695         [redacted]2   19990921        JP 1996-50[redacted]     19960802
     NO 9800450          A             19980401        NO 1998-450              19980202
PRIORITY APPLN. INFO.:                                 GB 1995-15941            19950803
                                                       WO 1996-GB1883           19960802


=> d 125 1-10 abs ibib

L25 HAS NO ANSWERS
'1-10 ' IS NOT A VALID SEARCH STATUS KEYWORD
Search status keywords:
NONE ---- Display only the number of postings.
STATUS -- Display statistics of the search.
ENTER SEARCH STATUS OPTION (NONE), STATUS, OR ?:

ENTER SEARCH STATUS OPTION (NONE), STATUS, OR ?:d 126 1-10 abs ibib

'D L130 1-10 ABS IBIB' IS NOT A VALID SEARCH STATUS KEYWORD
Search status keywords:
NONE ---- Display only the number of postings.
STATUS -- Display statistics of the search.
ENTER SEARCH STATUS OPTION (NONE), STATUS, OR ?:none

L2        199155 SEA PROMOTER
L12           13 SEA IACC
L25            0 SEA L12(P) L2


=> d his


     (FILE 'HOME' ENTERED AT 14:20:45 ON 21 JAN 2001)

     FILE 'CAPLUS, BIOSIS, CABA, CEABA-VTB' ENTERED AT 14:21:27 ON 21 JAN 2001
L1          1274 S MALATE(W)SYNTHASE
L2        199155 S PROMOTER
L3           203 S GERMIN
L4           877 S GLYOXYSOMAL
L5             0 S ALEUTRONE(W)LAYER
L6             0 S ALEUTRONE
L7         13735 S CARBOXYPEPTIDASE
L8          8459 S GLUTATHIONE(W)TRANSFERASE
L9           478 S ALCA
L10          186 S ALCR
L11            0 S IACC(P)REPRESSOR
L12           13 S IACC
L13         6132 S 434
L14         4174 S P22
L15         3352 S TET
L16        21064 S REPRESSOR
L17          459 S LAMBDA(W)BACTERIOPHAGE
L18           44 S L1(P)L2
L19           17 S L3(P)L2
L20           14 S L4(P)L2
L21          170 S L7(P)L2
L22           72 S L8(P)L2
L23           84 S L9(P)L2
L24           36 S L10(P)L2
L25            0 S L12(P)L2
L26          356 S L13(P)L16
L27          289 S L14(P)L16
L28          419 S L15(P)L16
L29           12 S L17(P)L16
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=> d l26 1-10 abs ibib

L26 ANSWER 1 OF 356 CAPLUS COPYRIGHT 2001 ACS

AB A dimer of the **434 repressor** bound at OR2 activated transcription initiation from PRM by contacting RNA polymerase. Although DNA-binding site mutations at either end of OR2 decreased the ability of the **repressor** to activate PRM transcription, mutations proximal to the promoter had a greater effect on transcription activation. Orienting a **repressor** subunit bearing the altered specificity Gln-28.fwdarw. Ala mutation to the half-site of OR2 proximal to the PRM promoter decreased the **repressor**'s ability to activate transcription initiation at **434** PRM to a much greater extent than if this subunit was placed in the OR2 half-site distal to PRM. In addn. to showing that the downstream (promoter proximal) subunit of the OR2-bound **434 repressor** functions in activating **434** PRM, the results indicated that DNA sequence-dependent conformational changes alter the efficiency with which the **repressor** activates PRM transcription. These unexpected findings highlight the importance of the structure of the **repressor**-DNA interface in activating transcription from PRM.

ACCESSION NUMBER: 2000:776906 CAPLUS
TITLE: DNA sequence requirements for the activation of **434** PRM transcription by **434 repressor**
AUTHOR(S): Xu, Jian; Koudelka, Gerald B.
CORPORATE SOURCE: Department of Biological Sciences, State University of New York at Buffalo, Buffalo, NY, USA
SOURCE: DNA Cell Biol. (2000), 19(10), 621-630
CODEN: DCEBE8; ISSN: 1044-5498
PUBLISHER: Mary Ann Liebert, Inc.
DOCUMENT TYPE: Journal
LANGUAGE: English
REFERENCE COUNT: 30
REFERENCE(S):
(1) Aggarwal, A; Science 1988, V242, P899 CAPLUS
(3) Bell, A; J Biol Chem 1995, V270, P1205 CAPLUS
(4) Bell, A; J Mol Biol 1993, V234, P542 CAPLUS
(5) Brunelle, A; Nucleic Acids Res 1985, V13, P5019 CAPLUS
(6) Busby, S; Cell 1994, V79, P743 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L26 ANSWER 2 OF 356 CAPLUS COPYRIGHT 2001 ACS

AB Folding kinetics for phage **434** Cro protein are examd. and compared with those reported for .lambda.6-85, the N-terminal domain of the **repressor** of phage .lambda.. The two proteins have similar all-helical structures consisting of five helixes but different stabilities. In contrast to .lambda.6-85, sharp and distinct arom. 1H NMR signals without exchange broadening characterize the native and urea-denatured **434** Cro forms at equil. at 20.degree., indicating slow interconversion on the NMR time scale. Stopped-flow fluorescence data using the single **434** Cro tryptophan indicate strongly urea-dependent refolding rates and smaller urea dependencies of the unfolding rates, suggesting a native-like transition state ensemble. Refolding rates are slower and unfolding rates considerably faster at pH 4 than at pH 6. This accounts for the lower stability of **434** Cro at pH 4 and suggests the existence of pH-dependent, possibly salt bridge interactions that are more stabilizing at pH 6. At <2 M urea, decreased folding amplitudes and nonlinear urea dependencies that are apparent at pH 6 indicate deviation from two-state behavior and suggest the formation of an early folding intermediate. The folding behavior of **434** Cro

and why it fold[redacted] orders of magnitude slower th[redacted].lambda.6-85 are rationalized in[redacted]rms of the lower intrinsic hel[redacted] stabilities and putative charge interactions in **434** Cro.

ACCESSION NUMBER: 2000:742726 CAPLUS
DOCUMENT NUMBER: 134:52864
TITLE: Folding Kinetics of Phage 434 Cro Protein
AUTHOR(S): Laurents, D. V.; Corrales, S.; Elias-Arnanz, M.; Sevilla, P.; Rico, M.; Padmanabhan, S.
CORPORATE SOURCE: Instituto de Estructura de la Materia, Consejo Superior de Investigaciones Cientificas, Madrid, 28006, Spain
SOURCE: Biochemistry (2000), 39(45), 13963-13973
CODEN: BICHAW; ISSN: 0006-2960
PUBLISHER: American Chemical Society
DOCUMENT TYPE: Journal
LANGUAGE: English
REFERENCE COUNT: 68
REFERENCE(S):
(1) Baldwin, R; Trends Biochem Sci 1999, V24, P77 CAPLUS
(2) Bax, A; J Magn Reson 1985, V65, P355 CAPLUS
(3) Bieri, O; Biochemistry 1999, V38, P12460 CAPLUS
(4) Burton, R; Biochemistry 1998, V37, P5337 CAPLUS
(5) Burton, R; Nat Sruct Biol 1997, V4, P305 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L26 ANSWER 3 OF 356 CAPLUS COPYRIGHT 2001 ACS
AB A review with 58 refs. The binding of proteins to specific DNA sequences plays a central role in the regulation of gene expression. Crucial to understanding how these proteins exert their effects is insight into the structure and flexibility of the protein-DNA complex. Over the past several years much has been learned about how the intimate contacts made between proteins and DNA enable proteins to recognize and bind with high specificity only to their cognate DNA binding sites. Studies conducted in our lab. have shown that sequence-specific binding of DNA by proteins not only involves the close approach of amino acids and base pairs in the binding site, but also that base pairs not in contact with the protein affect binding and specificity through sequence-specific effects on DNA structure. The direct reading of the DNA sequence by proteins occurs by chem. complementarity between the interacting groups. Proper alignment of the interacting surfaces of functional groups on the protein and DNA mols. is crucial to the formation of stable and specific protein-DNA complexes. In many cases, the appropriate juxtaposition of the chem. complementary groups requires mutual adjustments in the structure of protein and DNA. Failure to do so can result in loss of affinity, loss of specificity or both. Together, the dimer interface and non-contacted bases within or adjacent to the binding site direct the structural complementarity between the functional groups on the protein and DNA.

ACCESSION NUMBER: 2000:647147 CAPLUS
DOCUMENT NUMBER: 134:52662
TITLE: Role of the N- and C- terminal dimer interfaces of **434 repressor** in recognizing sequence-dependent DNA structure
AUTHOR(S): Koudelka, Gerald B.; Donner, Amy L.; Ciubotaru, Mihai
CORPORATE SOURCE: Department of Biological Sciences, State University of New York at Buffalo, Buffalo, NY, 14260, USA
SOURCE: Proc. Conversation Biomol. Stereodyn., 11th (2000), Volume Convers. 11, Issue 1, 135-139. Editor(s): Sarma, Ramaswamy H.; Sarma, Mukti H. Adenine Press: Schenectady, N. Y.
CODEN: 69AJOA

DOCUMENT TYPE: Conference; General Review
LANGUAGE: English
REFERENCE COUNT: 58
REFERENCE(S):
(1) Aggarwal, A; Science 1988, V242, P899 CAPLUS
(3) Anderson, J; Proc Natl Acad Sci USA 1984, V81, P1307 CAPLUS
(5) Benson, N; Mol Micro 1994, V11, P567 CAPLUS
(6) Carlson, P; J Bacteriol 1994, V176, P6907 CAPLUS
(7) Chakraborty, T; Mol Cell Biol 1991, V11, P3633 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L26 ANSWER 4 OF 356 CAPLUS COPYRIGHT 2001 ACS
AB The yeast two-hybrid system has been used to characterize many protein-protein interactions. A two-hybrid system for E. coli was constructed in which one hybrid protein bound to a specific DNA site recruits another to an adjacent DNA binding site. The first hybrid comprises a test protein, the bait, fused to a chimeric protein contg. the **434 repressor** DNA binding domain. In the second hybrid, a second test protein, the prey, is fused downstream of a chimeric protein with the DNA binding specificity of the .lambda. **repressor**. Reporters were designed to express cat and lacZ under the control of a low-affinity .lambda. operator. At low expression levels, .lambda. **repressor** hybrids weakly repress the reporter genes. A high-affinity operator recognized by **434 repressor** was placed nearby, in a position that does not yield repression by **434 repressor** alone. If the test proteins interact, the **434** hybrid bound to the **434** operator stabilizes the binding of the .lambda. **repressor** hybrid to the .lambda. operator, causing increased repression of the reporter genes. Reconstruction expts. with the fos and jun leucine zippers detected protein-protein interactions between either homodimeric or heterodimeric leucine zippers.
ACCESSION NUMBER: 2000:568999 CAPLUS
DOCUMENT NUMBER: 134:25830
TITLE: Two-hybrid system for characterization of protein-protein interactions in E. coli
AUTHOR(S): Hays, Lori B.; Chen, Yuen-Shing A.; Hu, James C.
CORPORATE SOURCE: Texas A and M University, College Station, TX, USA
SOURCE: BioTechniques (2000), 29(2), 288, 290, 292, 294, 296
CODEN: BTNQDO; ISSN: 0736-6205
PUBLISHER: Eaton Publishing Co.
DOCUMENT TYPE: Journal
LANGUAGE: English
REFERENCE COUNT: 33
REFERENCE(S):
(1) Allen, J; Trends Biochem Sci 1995, V20, P511 CAPLUS
(2) Bai, C; Methods Enzymol 1996, V273, P331 CAPLUS
(5) Beckett, D; Biochemistry 1993, V32, P9073 CAPLUS
(6) Brent, R; Ann Rev Genet 1997, V31, P663 CAPLUS
(7) Bunker, C; Nucleic Acids Res 1995, V23, P269 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L26 ANSWER 5 OF 356 CAPLUS COPYRIGHT 2001 ACS
AB A new set of stiffness parameters for all the 32 trinucleotide units has been set up directly from the three dimensional structures of DNA mols. It was obsd. that GAC/GTC is the stiffest trinucleotide and ACC/GGT is the most flexible one. The av. stiffness values computed for a set of operator sequences using the new parameters correlate very well with the protein-DNA binding specificity and binding free energy change of **434 repressor** and Cro **repressor**, resp. The new structure based stiffness scale can explain the protein-DNA binding

specificity to the level of 0.92.

ACCESSION NUMBER: 2000:354853 CAPLUS
DOCUMENT NUMBER: 133:292474
TITLE: Structure based sequence dependent stiffness scale for trinucleotides: a direct method
AUTHOR(S): Gromiha, M. Michael
CORPORATE SOURCE: Tsukuba Life Science Center, The Institute of Physical and Chemical Research (RIKEN), Tsukuba, 305-0074, Japan
SOURCE: J. Biol. Phys. (2000), 26(1), 43-50
CODEN: JBPHBZ; ISSN: 0092-0606
PUBLISHER: Kluwer Academic Publishers
DOCUMENT TYPE: Journal
LANGUAGE: English
REFERENCE COUNT: 37
REFERENCE(S):
(1) Barkley, M; J Chem Phys 1979, V70, P2991 CAPLUS
(2) Bauer, W; Proc Natl Acad Sci USA 1993, V90, P833 CAPLUS
(3) Bernstein, F; J Mol Biol 1977, V112, P535 CAPLUS
(4) Brukner, I; EMBO J 1995, V14, P1812 CAPLUS
(5) Brukner, I; J Biomol Str Dyn 1995, V13, P309 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L26 ANSWER 6 OF 356 CAPLUS COPYRIGHT 2001 ACS
AB Establishment and maintenance of a lysogen of the lambdoid bacteriophage **434** require that the **434 repressor** both activate transcription from the PRM promoter and repress transcription from the divergent PR promoter. Several lines of evidence indicate that the **434 repressor** activates initiation of PRM transcription by occupying a binding site adjacent to the PRM promoter and directly contacting RNA polymerase. The overlapping architecture of the PRM and PR promoters suggests that an RNA polymerase bound at PR may repress PRM transcription initiation. Hence, part of the stimulatory effect of the **434 repressor** may be relief of interference between RNA polymerase binding to the PRM promoter and to the PR promoter. Consistent with this proposal, we show that the **repressor** cannot activate PRM transcription if RNA polymerase binds at PR prior to addn. of the **434 repressor**. However, unlike the findings with the related .lambda. phage, formation of RNA polymerase promoter complexes at PRM and at PR apparently are mutually exclusive. We find that the RNA polymerase-mediated inhibition of **repressor**-stimulated PRM transcription requires the presence of an open complex at PR. Taken together, these results indicate that establishment of an open complex at PR directly prevents formation of an RNA polymerase-PRM complex.

ACCESSION NUMBER: 2000:348670 CAPLUS
DOCUMENT NUMBER: 133:277083
TITLE: Mutually exclusive utilization of PR and PRM promoters in bacteriophage 434 OR
AUTHOR(S): Xu, Jian; Koudelka, Gerald B.
CORPORATE SOURCE: Department of Biological Sciences, State University of New York at Buffalo, Buffalo, NY, 14260, USA
SOURCE: J. Bacteriol. (2000), 182(11), 3165-3174
CODEN: JOBAAY; ISSN: 0021-9193
PUBLISHER: American Society for Microbiology
DOCUMENT TYPE: Journal

LANGUAGE: English
REFERENCE COUNT: 28
REFERENCE(S):
(1) Bushman, F; Cell 1988, V54, P191 CAPLUS
(2) Bushman, F; J Mol Biol 1993, V230, P28 CAPLUS
(3) Bushman, F; Proc Natl Acad Sci USA 1986, V83, P9353 CAPLUS
(4) Choy, H; Proc Natl Acad Sci USA 1993, V90, P472 CAPLUS
(5) Dove, S; Nature 1997, V386, P627 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L26 ANSWER 7 OF 356 CAPLUS COPYRIGHT 2001 ACS
AB Combinatorial mutant libraries of the single-chain **434** **repressor** were used to discover novel DNA-binding specificities. Members of the library contain one wild type domain and one mutant domain which are connected by a recombinant peptide linker. The mutant domain contains randomized amino acids in place of the DNA-contacting residues. The single-chain derivs. are expected to recognize artificial operators contg. the DNA sequence of ACAA - 6 base-pairs - NNNN, where ACAA is bound by the wild-type and NNNN by the mutant domain. An in vivo library screening method was used to isolate mutant DNA-binding domains which recognize the TTAA site of an asym. operator. Several mutants showed high affinity binding to the selection target and also strong (up to 80 fold) preference for TTAA over the wild type TTGT sequence. Some of the isolated mutants bound with very high affinities (10 to 50 pM) to operators contg. the TTAC sequence, a close homolog of the TTAA selection target.
ACCESSION NUMBER: 2000:263849 CAPLUS
DOCUMENT NUMBER: 133:277811
TITLE: Single-chain 434 repressors with altered DNA-binding specificities: Isolation of mutant single-chain repressors by phenotypic screening of combinatorial mutant libraries
AUTHOR(S): Simoncsits, A.; Tjornhammar, M.-L.; Wang, S.; Pongor, S.
CORPORATE SOURCE: International Centre for Genetic Engineering and Biotechnology (ICGEB), Trieste, I-34012, Italy
SOURCE: NATO Sci. Ser., 3 (1999), 71(Structural Biology and Functional Genomics), 133-145
CODEN: NSSTFF; ISSN: 1388-6576
PUBLISHER: Kluwer Academic Publishers
DOCUMENT TYPE: Journal
LANGUAGE: English
REFERENCE COUNT: 28
REFERENCE(S):
(1) Aggarwal, A; Science 1988, V242, P899 CAPLUS
(2) Berg, J; Nature Biotech 1997, V15, P323 CAPLUS
(3) Berg, J; Science 1996, V271, P1081 CAPLUS
(4) Chen, J; Nucleic Acids Res 1997, V25, P2047 CAPLUS
(5) Choo, Y; Curr Opin Biotechnol 1995, V6, P431 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L26 ANSWER 8 OF 356 CAPLUS COPYRIGHT 2001 ACS
AB The plasmid pIP501 encoded transcriptional **repressor** CopR is one of the two regulators of plasmid copy no. CopR binds as a dimer to a nearly palindromic operator with the consensus sequence 5'-CGTG. Intermediate sequence searches revealed a significant structural relationship between CopR and the bacteriophage P22 c2 and the **434** c1 repressors. In this report we describe the exptl. verification of a CopR homol. model, which is based on a fairly low-sequence identity of 13.8% to P22 c2 **repressor**. A model for the complex of CopR with the DNA target was built on the basis of exptl. footprinting data, the

above-mentioned CopR homol. model, and the crystal structure of the **434** c1 **repressor**-DNA complex. Site-directed mutagenesis was used to test the function of amino acids involved in sequence and nonsequence-specific DNA recognition and amino acids important for correct protein folding. CD measurements were performed to detect structural changes caused by the mutations. Exchanges of residues responsible for sequence-specific DNA recognition reduced binding to a nonspecific level. Mutations of amino acids involved in nonspecific DNA binding lead to decreased binding affinity while maintaining selectivity. Substitution of amino acids necessary for proper folding caused dramatic structural changes. The exptl. data support the model of CopR as a helix-turn-helix protein belonging to the .lambda. **repressor** superfamily.

ACCESSION NUMBER: 2000:146511 CAPLUS
DOCUMENT NUMBER: 132:247694
TITLE: Transcriptional repressor CopR: structure model-based localization of the deoxyribonucleic acid binding motif
AUTHOR(S): Steinmetzer, Katrin; Hillisch, Alexander; Behlke, Joachim; Brantl, Sabine
CORPORATE SOURCE: Institut fur Molekularbiologie, Friedrich-Schiller-Universitat Jena, Jena, D-07745, Germany
SOURCE: Proteins: Struct., Funct., Genet. (2000), 38(4), 393-406
CODEN: PSFGEY; ISSN: 0887-3585
PUBLISHER: Wiley-Liss, Inc.
DOCUMENT TYPE: Journal
LANGUAGE: English
REFERENCE COUNT: 45
REFERENCE(S):
(2) Altschul, S; J Mol Biol 1990, V215, P403 CAPLUS
(3) Behlke, J; Biochemistry 1997, V36, P5149 CAPLUS
(4) Brantl, S; J Bacteriol 1997, V179, P7016 CAPLUS
(5) Brantl, S; Mol Microbiol 1994, V14, P473 CAPLUS
(6) Brantl, S; Nucleic Acids Res 1990, V18, P4783 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L26 ANSWER 9 OF 356 CAPLUS COPYRIGHT 2001 ACS
AB Combinatorial mutant libraries of the single-chain **434** **repressor** were used to discover novel DNA-binding specificities. Members of the library contain one wild type domain and one mutant domain which are connected by a recombinant peptide linker. The mutant domain contains randomized amino acids in place of the DNA-contacting residues. The single-chain derivs. are expected to recognize artificial operators contg. the DNA sequence of ACAA - 6 base-pairs - NNNN, where ACAA is bound by the wild-type and NNNN by the mutant domain. An in vivo library screening method was used to isolate mutant DNA-binding domains which recognize the TTAA site of an asym. operator. Several mutants showed high affinity binding to the selection target and also strong (up to 80 fold) preference for TTAA over the wild type TTGT sequence. Some of the isolated mutants bound with very high affinities (10-50 pM) to operators contg. the TTAC sequence, a close homolog of the TTAA selection target.

ACCESSION NUMBER: 2000:92882 CAPLUS
DOCUMENT NUMBER: 133:54264
TITLE: Single-chain 434 repressors with altered DNA-binding specificities: Isolation of mutant single-chain repressors by phenotypic screening of combinatorial mutant libraries
AUTHOR(S): Simoncsits, A.; Tjornhammar, M.-L.; Wang, S.; Pongor, S.
CORPORATE SOURCE: International Centre for Genetic Engineering and Biotechnology (ICGEB), Trieste, I-34012, Italy

SOURCE: Genetica (The Hague) (1999), 106(1-2), 85-92
CODEN: GENEA3; ISSN: 0016-67[redacted]
PUBLISHER: Kluwer Academic Publishers
DOCUMENT TYPE: Journal
LANGUAGE: English
REFERENCE COUNT: 28
REFERENCE(S):
(1) Aggarwal, A; Science 1988, V242, P899 CAPLUS
(2) Berg, J; Nature Biotech 1997, V15, P323 CAPLUS
(3) Berg, J; Science 1996, V271, P1081 CAPLUS
(4) Chen, J; Nucleic Acids Res 1997, V25, P2047 CAPLUS
(5) Choo, Y; Curr Opin Biotechnol 1995, V6, P431 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L26 ANSWER 10 OF 356 CAPLUS COPYRIGHT 2001 ACS
AB An artificial HIV-1 enhancer-binding 42-residue peptide (R42) that had been derived from bacteriophage **434 repressor** inhibited the cell-free in vitro transcription of HIV-1 enhancer-contg. plasmids. Here the authors show that, after N-terminal extension of R42 with a viral nuclear localization signal, the resulting nucR42 peptide was active in intact cells. NucR42 could be detected immunol. in nuclear exts. and produced a 60-70% redn. of the rate of transcription of an HIV-1 enhancer-carrying plasmid in COS-1 cells that had been cotransfected with the HIV enhancer plasmid, an expression plasmid for nucR42, and a control. NucR42 was also synthesized chem. and the synthetic product characterized by HPLC, mass spectrometry, and quant. amino acid anal. Band shift, footprint, and in vitro transcription assays in the presence of exogenous NF-.kappa.Bp50 indicated that the binding sites of nucR42 and NF-.kappa.B on the HIV enhancers overlapped and that a relatively small excess of nucR42 sufficed to displace NF-.kappa.Bp50. Band shift and in vitro transcription expts. showed also that exchange of the **434 repressor**-derived nine-residue recognition helix of nucR42 for four glycines abolished the HIV enhancer binding specificity whereas leucine zipper- or retro-leucine zipper-mediated dimerization of R42 analogs increased it suggesting the potential application of such dimeric HIV enhancer-binding peptides as intracellular inhibitors of HIV replication.
ACCESSION NUMBER: 1999:776699 CAPLUS
DOCUMENT NUMBER: 132:131825
TITLE: Inhibition of HIV-1 enhancer-controlled transcription by artificial enhancer-binding peptides derived from bacteriophage **434 repressor**
AUTHOR(S): Caderas, Georg; Klauser, Stephan; Liu, Niankun; Bienz, Alexander; Gutte, Bernd
CORPORATE SOURCE: Biochemisches Institut der Universitat Zurich, Zurich, CH-8057, Switz.
SOURCE: Eur. J. Biochem. (1999), 266(2), 599-607
CODEN: EJBCAI; ISSN: 0014-2956
PUBLISHER: Blackwell Science Ltd.
DOCUMENT TYPE: Journal
LANGUAGE: English
REFERENCE COUNT: 54
REFERENCE(S):
(1) Aggarwal, A; Science 1988, V242, P899 CAPLUS
(2) Anderson, J; Nature 1987, V326, P846 CAPLUS
(5) Burnette, W; Anal Biochem 1981, V112, P195 CAPLUS
(8) Choo, Y; Nature 1994, V372, P642 CAPLUS
(9) Chung, C; Methods Enzymol 1993, V218, P621 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

=> d l27 1-10 abs ib

L27 ANSWER 1 OF 289 CAPLUS COPYRIGHT 2001 ACS
AB The tetrameric Mnt **repressor** of bacteriophage **P22** consists of two dimeric DNA-binding domains and a tetramerization domain. The NOE and chem. shift data demonstrate that the structures of the domains in the wild-type **repressor** protein are similar to those of the sep. domains, the three-dimensional structures of which have been detd. previously. 15N relaxation measurements show that the linker that connects the anti-parallel four-helix bundle with the two .beta.-sheet DNA-binding dimers is highly flexible. No evidence was found for interactions between the distinct modules. The 15N relaxation properties of the two domains differ substantially, confirming their structural independence. A model in which one two-stranded coiled coil of the four-helix bundle is attached to one N-terminal dimer is most consistent with the biochem. data and 15N relaxation data. For the Mnt-DNA complex this geometry fits with a model in which the two .beta.-sheet DNA-binding domains are bound at two successive major grooves of the Mnt operator and the tetramerization domain is packed between these two DNA-bound dimers. In such a model the two-fold symmetry axis of the four-helix bundle coincides with that of the operator sequence and the two bound dimers. Bending of the Mnt operator of approx. 30.degree. upon binding of the tetramer, as measured by gel-shift assays, is in agreement with this model of the Mnt-DNA complex.

ACCESSION NUMBER: 2000:647145 CAPLUS
TITLE: Structure and dynamics of the tetrameric Mnt repressor and a model for its DNA complex
AUTHOR(S): Nooren, Irene M. A.; Folkers, Gert E.; Kaptein, Robert; Sauer, Robert T.; Boelens, Rolf
CORPORATE SOURCE: Department of NMR Spectroscopy, Bijvoet Center for Biomolecular Research, Utrecht University, Utrecht, 3584 CH, Neth.
SOURCE: Proc. Conversation Biomol. Stereodyn., 11th (2000), Volume Convers. 11, Issue 1, 113-122. Editor(s): Sarma, Ramaswamy H.; Sarma, Mukti H. Adenine Press: Schenectady, N. Y.
CODEN: 69AJOA
DOCUMENT TYPE: Conference
LANGUAGE: English
REFERENCE COUNT: 42
REFERENCE(S): (2) Blackledge, M; J Am Chem Soc 1998, V120, P4538 CAPLUS
(3) Bonvin, A; J Mol Biol 1994, V236, P328 CAPLUS
(4) Breg, J; Nature 1990, V346, P586 CAPLUS
(6) Brown, B; Biochemistry 1990, V29, P11189 CAPLUS
(8) Burgering, M; Biochemistry 1994, V33, P15036 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L27 ANSWER 2 OF 289 CAPLUS COPYRIGHT 2001 ACS
AB A solvent-exposed Cys11-Cys11' disulfide bond was designed to link the antiparallel strands of the .beta. sheet both in the Arc repressor dimer and in a single-chain variant in which the Arc subunits are connected by a 15-residue peptide tether. In both proteins, the presence of the disulfide bond increased the Tm by approx. 40.degree.. In the single-chain background, the disulfide bond stabilized Arc by 8.5 kcal/mol relative to the reduced form, a significantly larger degree of stabilization than caused by other engineered disulfides and most natural disulfides. This exceptional stabilization arises from a modest effective

concn. of the C[redacted]11-Cys11' disulfide in the nati[redacted] state (71 M) and an anomalously lo[redacted]ffective concn. in the denature[redacted]tate (40 .mu.M). Disulfide crosslinking of the two .beta. strands in the single-chain Arc background accelerated refolding by a factor of 170 into the sub-microsecond time scale. However, the major energetic effect of the disulfide occurs after the transition state for Arc refolding, slowing unfolding by 200 000-fold.

ACCESSION NUMBER: 2000:644437 CAPLUS
DOCUMENT NUMBER: 133:360183
TITLE: Striking Stabilization of Arc Repressor by an Engineered Disulfide Bond
AUTHOR(S): Robinson, Clifford R.; Sauer, Robert T.
CORPORATE SOURCE: Department of Biology, Massachusetts Institute of Technology, Cambridge, MA, 02139, USA
SOURCE: Biochemistry (2000), 39(40), 12494-12502
CODEN: BICHAW; ISSN: 0006-2960
PUBLISHER: American Chemical Society
DOCUMENT TYPE: Journal
LANGUAGE: English
REFERENCE COUNT: 47
REFERENCE(S): (1) Betz, S; Biochemistry 1992, V31, P12337 CAPLUS
(2) Betz, S; Biochemistry 1996, V35, P7422 CAPLUS
(3) Bonvin, A; J Mol Biol 1994, V236, P328 CAPLUS
(4) Bowie, J; Biochemistry 1989, V28, P7139 CAPLUS
(5) Bowie, J; J Biol Chem 1989, V264, P7596 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L27 ANSWER 3 OF 289 CAPLUS COPYRIGHT 2001 ACS
AB The plasmid pIP501 encoded transcriptional **repressor** CopR is one of the two regulators of plasmid copy no. CopR binds as a dimer to a nearly palindromic operator with the consensus sequence 5'-CGTG. Intermediate sequence searches revealed a significant structural relationship between CopR and the bacteriophage **P22** c2 and the 434 c1 repressors. In this report we describe the exptl. verification of a CopR homol. model, which is based on a fairly low-sequence identity of 13.8% to **P22** c2 **repressor**. A model for the complex of CopR with the DNA target was built on the basis of exptl. footprinting data, the above-mentioned CopR homol. model, and the crystal structure of the 434 c1 **repressor**-DNA complex. Site-directed mutagenesis was used to test the function of amino acids involved in sequence and nonsequence-specific DNA recognition and amino acids important for correct protein folding. CD measurements were performed to detect structural changes caused by the mutations. Exchanges of residues responsible for sequence-specific DNA recognition reduced binding to a nonspecific level. Mutations of amino acids involved in nonspecific DNA binding lead to decreased binding affinity while maintaining selectivity. Substitution of amino acids necessary for proper folding caused dramatic structural changes. The exptl. data support the model of CopR as a helix-turn-helix protein belonging to the .lambda. **repressor** superfamily.

ACCESSION NUMBER: 2000:146511 CAPLUS
DOCUMENT NUMBER: 132:247694
TITLE: Transcriptional repressor CopR: structure model-based localization of the deoxyribonucleic acid binding motif
AUTHOR(S): Steinmetzer, Katrin; Hillisch, Alexander; Behlke, Joachim; Brantl, Sabine
CORPORATE SOURCE: Institut fur Molekularbiologie, Friedrich-Schiller-Universitat Jena, Jena, D-07745, Germany
SOURCE: Proteins: Struct., Funct., Genet. (2000), 38(4), 393-406
CODEN: PSFGEY; ISSN: 0887-3585
PUBLISHER: Wiley-Liss, Inc.
DOCUMENT TYPE: Journal

LANGUAGE: English
REFERENCE COUNT: 45
REFERENCE(S):
(2) Altschul, S; J Mol Biol 1990, V215, P403 CAPLUS
(3) Behlke, J; Biochemistry 1997, V36, P5149 CAPLUS
(4) Brantl, S; J Bacteriol 1997, V179, P7016 CAPLUS
(5) Brantl, S; Mol Microbiol 1994, V14, P473 CAPLUS
(6) Brantl, S; Nucleic Acids Res 1990, V18, P4783 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L27 ANSWER 4 OF 289 CAPLUS COPYRIGHT 2001 ACS
AB The structure and dynamics of the chymotryptic tetramerization domain of the Mnt **repressor** of Salmonella bacteriophage **P22** have been studied by NMR spectroscopy. Two sets of resonances (A and B) were found, representing the asymmetry within the homotetramer. Triple-resonance techniques were used to obtain unambiguous assignments of the A and B resonances. Intra-monomeric NOEs, which were distinguished from the inter-monomeric NOEs by exploiting 13C/15N-filtered NOE expts., demonstrated a continuous .alpha.-helix of approx. seven turns for both the A and B monomers. The asymmetry facilitated the interpretation of inter-subunit NOEs, whereas the antiparallel alignment of the subunits allowed further discrimination of inter-monomeric NOEs. The three-dimensional structure revealed an unusual asym. packing of a dimer of two antiparallel right-handed intertwined coiled .alpha.-helixes. The A and B forms exchange on a timescale of seconds by a mechanism that probably involves a relative sliding of the two coiled coils. The amide proton solvent exchange rates demonstrate a stable tetrameric structure. The essential role of Tyr 78 in oligomerization of Mnt, found by previous mutagenesis studies, can be explained by the many hydrophobic and hydrogen bonding interactions that this residue participates in with adjacent monomers.
ACCESSION NUMBER: 1999:710338 CAPLUS
DOCUMENT NUMBER: 132:32393
TITLE: NMR structure determination of the tetramerization domain of the Mnt repressor: an asymmetric .alpha.-helical assembly in slow exchange
AUTHOR(S): Nooren, Irene M. A.; George, Albert V. E.; Kaptein, Robert; Sauer, Robert T.; Boelens, Rolf
CORPORATE SOURCE: Department of NMR Spectroscopy, Bijvoet Center for Biomolecular Research, Utrecht University, Utrecht, 3584 CH, Neth.
SOURCE: J. Biomol. NMR (1999), 15(1), 39-53
CODEN: JBNME9; ISSN: 0925-2738
PUBLISHER: Kluwer Academic Publishers
DOCUMENT TYPE: Journal
LANGUAGE: English
REFERENCE COUNT: 44
REFERENCE(S):
(2) Bax, A; J Magn Reson 1985, V63, P207 CAPLUS
(3) Bothner-By, A; J Am Chem Soc 1984, V106, P811 CAPLUS
(4) Breg, J; Nature 1990, V346, P586 CAPLUS
(6) Burgering, M; Biochemistry 1994, V33, P15036 CAPLUS
(7) Burgering, M; FEBS Lett 1993, V330, P105 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L27 ANSWER 5 OF 289 CAPLUS COPYRIGHT 2001 ACS
AB The tetrameric Mnt **repressor** is involved in the genetic switch between the lysogenic and lytic growth of Salmonella bacteriophage **P22**. The soln. structure of its C-terminal tetramerization domain, which holds together the two dimeric DNA-binding domains, has been detd. by NMR spectroscopy. This structure reveals an assembly of four

.alpha.-helical subunits, consisting of a dimer of two antiparallel coiled coils with a unique right-handed twist. The superhelical winding is considerably stronger and the interhelical sepn. closer than those found in the well-known left-handed coiled coils in fibrous proteins and leucine zippers. An unusual asymmetry arises between the two monomers that comprise one right-handed coiled coil. A difference in the packing to the adjacent monomer of the other coiled coil occurs with an offset of two helical turns. The two asym. monomers within each coiled coil interconvert on a time scale of seconds. Both with respect to symmetry and handedness of helical packing, the C2 sym. four-helix bundle of Mnt differs from other oligomerization domains that assemble DNA-binding modules, such as that in the tumor suppressor p53 and the E. coli lac **repressor**.

ACCESSION NUMBER: 1999:500206 CAPLUS
DOCUMENT NUMBER: 131:268555
TITLE: The tetramerization a domain of the Mnt repressor consists of two right-handed coiled coils
AUTHOR(S): Nooren, Irene M. A.; Kaptein, Robert; Sauer, Robert T.; Boelens, Rolf
CORPORATE SOURCE: Department of NMR Spectroscopy, Bijvoet Center for Biomolecular Research, Utrecht University, Utrecht, 3584 CH, Neth.
SOURCE: Nat. Struct. Biol. (1999), 6(8), 755-759
CODEN: NSBIEW; ISSN: 1072-8368
PUBLISHER: Nature America
DOCUMENT TYPE: Journal
LANGUAGE: English
REFERENCE COUNT: 32
REFERENCE(S):
(1) Bax, A; J Magn Reson 1985, V63, P207 CAPLUS
(2) Betz, S; Curr Opin Struct Biol 1995, V5, P457 CAPLUS
(4) Burgering, M; Biochemistry 1994, V33, P15036 CAPLUS
(5) Chothia, C; J Mol Biol 1981, V145, P215 CAPLUS
(6) Clore, G; Science 1995, V267, P1515 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L27 ANSWER 6 OF 289 CAPLUS COPYRIGHT 2001 ACS
AB The soln. structure of the hyperstable MYL mutant (R31M/E36Y/R40L) of the Arc **repressor** of bacteriophage **P22** was detd. by NMR spectroscopy and compared to that of the wild-type Arc **repressor**. A backbone rmsd vs. the av. of 0.37 .ANG. was obtained for the well-defined core region. For both Arc-MYL and the wild-type Arc **repressor**, evidence for a fast equil. between a packed ("in") conformation and an extended ("out") conformation of the side chain of Phe 10 was found. In the MYL mutant, the "out" conformation is more highly populated than in the wild-type Arc **repressor**. Phe 10 is situated in the DNA-binding .beta.-sheet of the Arc dimer. While its "in" conformation appears to be the most stable, the "out" conformation is known to be present in the operator-bound form of Arc, where the Phe 10 ring contacts the phosphate backbone [Raumann, B. E., et al. (1994) Nature 367, 754-757]. As well as DNA binding, denaturation by urea and high temps. induces the functionally active "out" conformation. With a repacking of the hydrophobic core, this characterizes a premelting transition of the Arc **repressor**. The dynamical properties of the Arc-MYL and the wild-type Arc **repressor** were further characterized by 15N relaxation and hydrogen-deuterium exchange expts. The increased main chain mobility at the DNA binding site compared to that of the core of the protein as well as the reorientation of the side chain of Phe 10 is suggested to play an important role in specific DNA binding.

ACCESSION NUMBER: 1999:255418 CAPLUS

DOCUMENT NUMBER: 131:69890
TITLE: The Solution Structure and Dynamics of an Arc Repressor Mutant Reveal Premelting Conformational Changes Related to DNA Binding
AUTHOR(S): Nooren, Irene M. A.; Rietveld, Alex W. M.; Melacini, Giuseppe; Sauer, Robert T.; Kaptein, Robert; Boelens, Rolf
CORPORATE SOURCE: Department of NMR Spectroscopy, Bijvoet Center for Biomolecular Research, Utrecht University, Utrecht, 3584 CH, Neth.
SOURCE: Biochemistry (1999), 38(19), 6035-6042
CODEN: BICHAW; ISSN: 0006-2960
PUBLISHER: American Chemical Society
DOCUMENT TYPE: Journal
LANGUAGE: English
REFERENCE COUNT: 30
REFERENCE(S):
(1) Bonvin, A; J Mol Biol 1994, V236, P328 CAPLUS
(2) Bothner-By, A; J Am Chem Soc 1984, V106, P811 CAPLUS
(3) Bowie, J; Biochemistry 1989, V28, P7139 CAPLUS
(4) Breg, J; Biochemistry 1989, V28, P9826 CAPLUS
(5) Breg, J; Nature 1990, V346, P586 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L27 ANSWER 7 OF 289 CAPLUS COPYRIGHT 2001 ACS
AB Hydrophobic substitutions at solvent-exposed positions in two .alpha.-helical regions of the bacteriophage **P22** Arc **repressor** were introduced by combinatorial mutagenesis. In helix A, hydrophobic residues were tolerated individually at each of the five positions examd., but multiple substitutions were poorly tolerated as shown by the finding that mutants with more than two addnl. hydrophobic residues were biol. inactive. Several inactive helix A variants were purified and found to have reduced thermal stability relative to wild-type Arc, with a rough correlation between the no. of polar-to-hydrophobic substitutions and the magnitude of the stability defect. Quite different results were obtained in helix B, where variants with as many as five polar-to-hydrophobic substitutions were found to be biol. active and one variant with three hydrophobic substitutions had a tm 6.degree. higher than wild-type. By contrast, a helix A mutant with three similar polar-to-hydrophobic substitutions was 23.degree. less stable than wild-type. Also, one set of three polar-to-hydrophobic substitutions in helix B was tolerated when introduced into the wild-type background but not when introduced into an equally active mutant having a nearly identical structure. Context effects occur both when comparing different regions of the same protein and when comparing the same region in two different homologs.
ACCESSION NUMBER: 1999:115596 CAPLUS
DOCUMENT NUMBER: 130:278269
TITLE: Tolerance of a protein to multiple polar-to-hydrophobic surface substitutions
AUTHOR(S): Cordes, Matthew H. J.; Sauer, Robert T.
CORPORATE SOURCE: Department of Biology, Massachusetts Institute of Technology, Cambridge, MA, 02139, USA
SOURCE: Protein Sci. (1999), 8(2), 318-325
CODEN: PRCIEI; ISSN: 0961-8368
PUBLISHER: Cambridge University Press
DOCUMENT TYPE: Journal
LANGUAGE: English
REFERENCE COUNT: 24
REFERENCE(S):
(1) Bowie, J; Biochemistry 1989, V28, P7139 CAPLUS
(2) Bowie, J; Proc Natl Acad Sci USA 1989, V86, P2152 CAPLUS
(3) Bowie, J; Science 1990, V247, P1306 CAPLUS
(4) Bowler, B; Biochemistry 1993, V32, P183 CAPLUS

(5) Brown, B; Biochemistry 19[redacted] V29, P11189 CAPLUS
ALL CITATIONS AVAILABLE IN TH[redacted]RE FORMAT

L27 ANSWER 8 OF 289 CAPLUS COPYRIGHT 2001 ACS
AB A central question in protein-DNA recognition is the origin of the specificity that permits binding to the correct site in the presence of excess, nonspecific DNA. In the **P22** Arc **repressor**, the Phe-10 side chain is part of the hydrophobic core of the free protein but rotates out to pack against the sugar-phosphate backbone of the DNA in the **repressor**-operator complex. Characterization of a library of position 10 variants reveals that Phe is the only residue that results in fully active Arc. One class of mutants folds stably but binds operator with reduced affinity; another class is unstable. FV10, one member of the first class, binds operator DNA and nonoperator DNA almost equally well. The affinity differences between FV10 and wild type indicate that each Phe-10 side chain contributes 1.5-2.0 kcal to operator binding but less than 0.5 kcal/mol to nonoperator binding, demonstrating that contacts between Phe-10 and the operator DNA backbone contribute to binding specificity. This appears to be a direct contribution as the crystal structure of the FV10 dimer is similar to wild type and the Phe-10-DNA backbone interactions are the only contacts perturbed in the cocrystal structure of the FV10-operator complex.
ACCESSION NUMBER: 1999:99182 CAPLUS
DOCUMENT NUMBER: 130:263643
TITLE: Origins of DNA-binding specificity: role of protein contacts with the DNA backbone
AUTHOR(S): Schildbach, Joel F.; Karzai, A. Wali; Raumann, Brigitte E.; Sauer, Robert T.
CORPORATE SOURCE: Department of Biology, Massachusetts Institute of Technology, Cambridge, MA, 02139-4307, USA
SOURCE: Proc. Natl. Acad. Sci. U. S. A. (1999), 96(3), 811-817
CODEN: PNASA6; ISSN: 0027-8424
PUBLISHER: National Academy of Sciences
DOCUMENT TYPE: Journal
LANGUAGE: English
REFERENCE COUNT: 26
REFERENCE(S): (1) Bonvin, A; J Mol Biol 1994, V236, P328 CAPLUS
(2) Bowie, J; Biochemistry 1989, V28, P7139 CAPLUS
(3) Bowie, J; J Biol Chem 1989, V264, P7596 CAPLUS
(4) Breg, J; Nature (London) 1990, V346, P586 CAPLUS
(5) Brown, B; Biochemistry 1990, V29, P11189 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L27 ANSWER 9 OF 289 CAPLUS COPYRIGHT 2001 ACS
AB The invention relates to a regulation system for inducible expression of genes, comprising a lambdoid promoter, a gene coding for a **repressor** for the lambdoid promotor and a gene coding for an antirepressor of the **repressor**, which antirepressor is under the influence of an inducible promotor. The invention further relates to a regulatory replicon, comprising said gene coding for an antirepressor, an expression system, comprising said regulatory replicon, and an expression vector based on a lambdoid promotor, and also to a method for producing a gene product in a heterologous host, by providing a culture of a host comprising a heterologous sequence which codes for the gene product, wherein the expression of the heterologous sequence is under the control of a regulation system, a gene coding for a **repressor** for the lambdoid promotor and a gene coding for an antirepressor, and by inducing the promotor of the antirepressor gene. Thus, a replicon (designated pICA2) is constructed comprising the gene coding for the Salmonella typhimurium phage **P22** ant protein under the control of the PN25/O2 promoter, the lacIq gene under the control of the pLacIq promoter,

and the gene coding for the cI857 **repressor**. The system is illustrated on the basis of the prokaryote lacZ gene and the eukaryote genes coding for human interferon-.gamma., murine interleukin 2, and human interleukin 2 as model systems for protein synthesis.

ACCESSION NUMBER: 1998:709194 CAPLUS
DOCUMENT NUMBER: 129:326951
TITLE: Regulatory system for inducible expression of genes with lambdoid promoters
INVENTOR(S): Mertens, Nico Maurice August Corneel; Remaut, Erik Rene; Fiers, Walter Charles
PATENT ASSIGNEE(S): Vlaams Interuniversitair Instituut Voor Biotechnologie, Belg.
SOURCE: PCT Int. Appl., 39 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9848025	A2	19981029	WO 1998-EP2465	19980423
WO 9848025	A3	19990121		
W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
AU 9876491	A1	19981113	AU 1998-76491	19980423
EP 975775	A2	20000202	EP 1998-924212	19980423
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
PRIORITY APPLN. INFO.:			NL 1997-1005884	19970423
			WO 1998-EP2465	19980423

L27 ANSWER 10 OF 289 CAPLUS COPYRIGHT 2001 ACS

AB The bacteriophage .lambda. **repressor** and its relatives bind cooperatively to adjacent as well as artificially sepd. operator sites. This cooperativity is mediated by a protein-protein interaction between the DNA-bound dimers. Here we use a genetic approach to identify two pairs of amino acids that interact at the dimer-dimer interface. One of these pairs is nonconserved in the aligned sequences of the .lambda. and **P22** repressors; we show that a .lambda. **repressor** variant bearing the **P22** residues at these two positions interacts specifically with the **P22 repressor**. The other pair consists of a conserved ion pair; we reverse the charges at these two positions and demonstrate that, whereas the individual substitutions abolish the interaction of the DNA-bound dimers, these changes in combination restore the interaction of both .lambda.cI and P22c2 dimers.

ACCESSION NUMBER: 1998:597224 CAPLUS
DOCUMENT NUMBER: 129:311620
TITLE: Amino acid-amino acid contacts at the cooperativity interface of the bacteriophage .lambda. and P22 repressors
AUTHOR(S): Whipple, Frederick W.; Hou, Emmeline F.; Hochschild, Ann
CORPORATE SOURCE: Dep. of Microbiology and Molecular Genetics, Harvard Medical School, Boston, MA, 02115, USA
SOURCE: Genes Dev. (1998), 12(17), 2791-2802
CODEN: GEDEEP; ISSN: 0890-9369

PUBLISHER: Cold Spring Harbor Laboratory Press
DOCUMENT TYPE: Journal
LANGUAGE: English

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L28 ANSWER 1 OF 419 CAPLUS COPYRIGHT 2001 ACS

AB A method for identifying transcriptional regulatory proteins that modulate the transcription of a gene of interest is disclosed. In one embodiment, the method comprises introducing into a cell a nucleic acid mol. comprising three central components: 1) a polynucleotide (e.g., DNA) encoding a transcriptional regulatory protein; 2) an indicator gene which is responsive to, e.g., under the transcriptional control of, the gene regulatory sequences of a gene of interest which bind to the transcriptional regulatory protein; and 3) a selectable marker gene. Here a fusion protein is engineered which contains a DNA binding domain and a transcriptional regulatory domain which bind to the gene regulatory sequences of interest. This involves expression of the **Tet repressor**-based regulatory protein and the tetracycline controlled transactivator (tTA) protein or a variant. Here tetracycline analogs comprisingdoxycycline, anhydrotetracycline, oxy-tetracycline and chloro-tetracycline may be used for induction. **Tet** operator sequences are engineered which have at least one substitution. The transcriptional regulatory protein binds to the gene regulatory sequences and either activates or inhibits transcription. A protein is identified as a modulator of the transcription of the gene of interest by detecting a signal generated by the indicator gene. The indicator gene may be green fluorescent protein or may induce cell growth or a second messenger system. Here a novel TetR-based transactivator-rtTA-34R was found. The mutations found in rtTA-34R are E19G, A56P, H139H, A148E, and H179R. Here, two exchanges E19G and A56P are sufficient for the reverse phenotype. This new reverse activator is a decisive improvement when compared to the previously characterized rtTA.

ACCESSION NUMBER: 2000:881349 CAPLUS
DOCUMENT NUMBER: 134:37906
TITLE: Method for identifying novel transcriptional regulatory proteins and presentation of improved **Tet repressor**-based regulatory protein
INVENTOR(S): Hillen, Wolfgang
PATENT ASSIGNEE(S): Germany
SOURCE: PCT Int. Appl., 70 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2000075362	A2	20001214	WO 2000-IB859	20000605

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

PRIORITY APPLN. INFO.: US 1999-137671 19990604

L28 ANSWER 2 OF 419 CAPLUS COPYRIGHT 2001 ACS

AB The present invention provides a panel of transcriptional activator fusion proteins which comprises both tetracycline controlled transactivator proteins and reverse tetracycline transactivator proteins. These modulate the tet operator and are expressed from an expression vector within the hosts of plant cells, insect cells, fungal cells, bacterial cells, mammalian cells or a virus. Antibodies are described which bind these proteins. These transactivators have novel phenotypes such as altered basal transcriptional activity in the absence of doxycycline, altered induced transcriptional activity in the presence of doxycycline, or differential induction by tetracycline and analogs of tetracycline. Mutations were introduced within the tetracycline binding domain of these proteins to mimic allele variants. These would confer altered basal affinity for the Tet operator in the absence of doxycycline. These could also confer increased or decreased sensitivity towards doxycycline. Gene therapy approaches involving these constructs were demonstrated.

ACCESSION NUMBER: 2000:881334 CAPLUS
DOCUMENT NUMBER: 134:52955
TITLE: Novel **tet repressor**-based transcriptional regulatory proteins with applications for gene therapy
INVENTOR(S): Hillen, Wolfgang; Bujard, Hermann
PATENT ASSIGNEE(S): Germany
SOURCE: PCT Int. Appl., 167 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2000075347	A2	20001214	WO 2000-IB886	20000605

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

PRIORITY APPLN. INFO.: US 1999-137986 19990607

L28 ANSWER 3 OF 419 CAPLUS COPYRIGHT 2001 ACS

AB Unavailable

ACCESSION NUMBER: 2000:850081 CAPLUS
TITLE: **Tet repressor**-based system for regulated gene expression in eukaryotic cells: principles and advances
AUTHOR(S): Baron, Udo; Bujard, Hermann
CORPORATE SOURCE: Zentrum fur Molekulare Biologie, Universitat Heidelberg, Heidelberg, D-69120, Germany
SOURCE: Methods Enzymol. (2000), 327(Applications of Chimeric Genes and Hybrid Proteins, Pt. B), 401-421
CODEN: MENZAU; ISSN: 0076-6879
PUBLISHER: Academic Press
DOCUMENT TYPE: Journal
LANGUAGE: English
REFERENCE COUNT: 31
REFERENCE(S): (1) Baron, U; Nucleic Acids Res 1997, V25, P2723 CAPLUS
(2) Baron, U; Proc Natl Acad Sci USA 1999, V96, P1013

CAPLUS
(5) Bell, A; Curr Opin Genet Dev 1999, V9, P191
CAPLUS
(6) Clement, J; RNA 1999, V5, P206 CAPLUS
(8) Deuschle, U; Mol Cell Biol 1995, V15, P1907
CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L28 ANSWER 4 OF 419 CAPLUS COPYRIGHT 2001 ACS
AB The complete nucleotide sequence of the tetracycline resistance plasmid pAG1 from the gram-pos. soil bacterium Corynebacterium glutamicum 22243 (formerly Corynebacterium melassecola 22243) was detd. The R-plasmid has a size of 19,751 bp and contains at least 18 complete open reading frames.
The resistance determinant of pAG1 revealed homol. to gram-neg. tetracycline efflux and **repressor** systems of **Tet** classes A through J. The highest levels of amino acid sequence similarity were obsd. to the transmembrane tetracycline efflux protein TetA(A) and to the tetracycline **repressor** TetR(A) of transposon Tn1721 with 64 and 56% similarity, resp. This is the first time a **repressor** -regulated **tet** gene has been found in gram-pos. bacteria. A new class of tetracycline resistance and **repressor** proteins, termed TetA(Z) and TetR(Z), is proposed. (c) 2000 Academic Press.
ACCESSION NUMBER: 2000:803231 CAPLUS
TITLE: TetZ, a New Tetracycline Resistance Determinant Discovered in Gram-Positive Bacteria, Shows High Homology to Gram-Negative Regulated Efflux Systems
AUTHOR(S): Tauch, Andreas; Puhler, Alfred; Kalinowski, Jorn; Thierbach, Georg
CORPORATE SOURCE: Degussa-Huls AG, Halle-Kunsebeck, D-33790, Germany
SOURCE: Plasmid (2000), 44(3), 285-291
CODEN: PLSMDX; ISSN: 0147-619X
PUBLISHER: Academic Press
DOCUMENT TYPE: Journal
LANGUAGE: English
REFERENCE COUNT: 19
REFERENCE(S): (1) Allard, J; J Bacteriol 1993, V175, P4554 CAPLUS
(2) Allmeier, H; Gene 1992, V111, P11 CAPLUS
(3) Altschul, S; Nucleic Acids Res 1997, V25, P3389 CAPLUS
(4) Grant, S; Proc Natl Acad Sci USA 1990, V87, P4645 CAPLUS
(5) Inouye, M; Gene 1994, V141, P39 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L28 ANSWER 5 OF 419 CAPLUS COPYRIGHT 2001 ACS
AB The invention provides a new system for antibiotic-regulated gene expression in eukaryotic cells based on sequences from Actinomycetes antibiotic resistance promoters, polypeptides that bind to the same in an antibiotic responsive manner, and nucleotides encoding such polypeptides. Further, the invention provides novel and sensitive methods of screening for candidate antibiotics. Use of transcriptional activators or repressors that bind to Pabr sequence, reporter gene, **tet** operator, internal ribosomal entry site (IRES), is claimed. Tumor suppressor gene sequence, sequence coding for a gene product that activates cell proliferation or a survival factor, are utilized also. Pabr-binding protein is derived from Streptomycete, Streptomyces coelicolor, in particular. We designed a new strategy for efficient regulation of cloned gene expression in mammalian cells. The new gene regulation system is responsive to streptogramins, a class of human therapy-proven antibiotics such as pristinamycin and virginiamycin, which are naturally produced by Streptomyces spp. The pristinamycin-responsive interaction between the **repressor** (Pip) of the pristinamycin resistance gene (ptr) and its target sequence, ptr promoter (PPTR) formed

the basis for construction of two chimeric genetic determinants: Pip was fused to a eukaryotic transactivator domain (PIT, pristinamycin-responsive transactivator) and the Pip binding DNA sequence (PPTR) was cloned 5' of a minimal insect promoter resulting in PPIR (pristinamycin I-responsive promoter). PIT retains its streptogramin-dependent PPTR binding capacity in mammalian cells which enables sufficiently close contact between the transactivation domain and the minimal promoter to achieve transcription initiation in absence of streptogramin antibiotics. In the presence of streptogramins, PIT is released from PPIR and gene expression is abolished. The novel PIT/PPIR system shows excellent regulation characteristics (high expression levels and low basal activity) in a variety of mammalian cell lines including CHO-K1, BHK-21 and HeLa cells. In addn., the streptogramin regulation system is compatible with the well-established tetracycline-responsive expression concept which enables the combined use of these two distinct systems in a single cell for independent control of different transgenes.

ACCESSION NUMBER: 2000:772781 CAPLUS
DOCUMENT NUMBER: 133:330524
TITLE: Mammalian gene expression regulation system responsive to streptogramin antibiotics
INVENTOR(S): Thompson, Charles J.; Bailey, James E.
PATENT ASSIGNEE(S): Fussenegger, Martin, Switz.
SOURCE: PCT Int. Appl., 66 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2000065080	A1	20001102	WO 2000-US11091	20000421

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

PRIORITY APPLN. INFO.: US 1999-298768 19990423
US 1999-411687 19991004

REFERENCE COUNT: 3
REFERENCE(S):
(1) Bujard; US 5589362 A 1996 CAPLUS
(2) Clackson, T; Current Opinions in Chemical Biology 1997, V1, P210 CAPLUS
(3) Guilfoile; Journal of Bacteriology 1992, V174(11), P3659 CAPLUS

L28 ANSWER 6 OF 419 CAPLUS COPYRIGHT 2001 ACS
AB Genetic manipulation techniques are widely used in mice to study the functions of genes. The most common strategy for assessing in vivo function involves making irreversible changes in the genome by homologous recombination. To complement this approach, a no. of systems have been developed that allow specific and controlled expression of a gene. One of the more versatile and promising systems is based on the tetracycline (**tet**) responsive bacterial tetracycline **repressor** (TetR). In recent years, the **tet** system has proven to be a valuable method for understanding the function of genes involved in a no. of

physiol. proces[redacted], including mouse models for h[redacted]n diseases such as cancer and neur[redacted] and pigment disorders. This [redacted]view will highlight the power and elegance of the **tet** system by focusing on its utility in the study of two pigment cell-related biol. problems, the pathogenesis of melanomas and melanocyte development in the embryo.

ACCESSION NUMBER: 2000:743365 CAPLUS
TITLE: Controlling gene expression in mice with tetracycline:
Application in pigment cell research
AUTHOR(S): Shin, Myung K.
CORPORATE SOURCE: Cell and Developmental Biology Program, Fox Chase Cancer Center, Philadelphia, PA, 19111, USA
SOURCE: Pigm. Cell Res. (2000), 13(5), 326-331
CODEN: PCREEA; ISSN: 0893-5785
PUBLISHER: Munksgaard International Publishers Ltd.
DOCUMENT TYPE: Journal
LANGUAGE: English
REFERENCE COUNT: 59
REFERENCE(S):
(1) Albanese, C; Faseb J 2000, V14, P877 CAPLUS
(2) Amiel, J; Hum Mol Genet 1996, V5, P355 CAPLUS
(3) Auricchio, A; Hum Mol Genet 1996, V5, P351 CAPLUS
(4) Baron, U; Nucleic Acids Res 1997, V25, P2723 CAPLUS
(5) Baron, U; Proc Natl Acad Sci USA 1999, V96, P1013 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L28 ANSWER 7 OF 419 CAPLUS COPYRIGHT 2001 ACS
AB We applied the bacterial lactose and tetracycline **repressor** -operator systems to an interleukin 2-dependent T-cell line, Kit 225, to examine the effects of the human T-cell leukemia virus type I oncogene product, Tax, on the cell cycle. The LacSwitch and **Tet**-Off inducible systems individually exhibited low expression of Tax upon induction in growing Kit 225 cells. In contrast, combination of the LacSwitch system with the **Tet**-Off system produced a high Tax expression level in growing Kit 225 cells; however when arrested at the G0/G1 phase of the cell cycle, Kit 225 cells expressed very low levels of Tax, assocd. with little or no cell cycle progression. Infection with the Tax recombinant adenovirus induced high expression of Tax and progression of the cell cycle. Our results indicate that the combined LacSwitch and **Tet**-Off systems may require cell growth for gene expression. (c) 2000 Academic Press.

ACCESSION NUMBER: 2000:717848 CAPLUS
TITLE: Requirement of Cell Growth for Gene Expression Induced
by the Lactose and Tetracycline Repressor-Operator Combination System in a Human T Cell Line
AUTHOR(S): Iwanaga, Ritsuko; Ohtani, Kiyoshi; Nakamura, Masataka
CORPORATE SOURCE: Human Gene Sciences Center, Tokyo Medical and Dental University, Bunkyo-ku, Tokyo, 113-8510, Japan
SOURCE: Biochem. Biophys. Res. Commun. (2000), 276(2), 546-552
CODEN: BBRCA9; ISSN: 0006-291X
PUBLISHER: Academic Press
DOCUMENT TYPE: Journal
LANGUAGE: English
REFERENCE COUNT: 22
REFERENCE(S):
(1) Brown, M; Cell 1987, V49, P603 CAPLUS
(2) Englert, C; EMBO J 1995, V14, P4662 CAPLUS
(3) Figge, J; Cell 1988, V52, P713 CAPLUS
(4) Gossen, M; Science 1995, V268, P1766 CAPLUS
(5) Hori, T; Blood 1987, V70, P1069 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L28 ANSWER 8 OF 419 CAPLUS COPYRIGHT 2001 ACS

AB Recombinant human U6 snRNA gene promoter that has the sequence between proximal sequence element and TATA box replaced by the sequence recognized by DNA binding proteins, is disclosed. Vectors contg. the recombinant promoter and desired RNA sequences, such as antisense RNA, ribozyme, or aptamer, as well as mammalian cells transfected with them, are claimed. Drugs, more specifically anticancer drugs contg. the vector, are also claimed. In an effort to develop a regulatable deriv. of the promoter of the human gene for U6 snRNA, we generated several constructs composed of the human U6 snRNA promoter and sequences derived from the gene for the tetracycline operator of a prokaryotic tetracycline resistance transposon. One of the constructs had strong transcriptional activity in the presence of tetracycline that was equiv. to 80% of the activity of the wild-type promoter. Furthermore, the transcriptional activity was almost completely repressed in the absence of tetracycline. Transcriptional activity became detectable within 4 h after the addn. of tetracycline to the culture medium. We used this system to control the functional activity of an antisense RNA for a chimeric gene derived from genes for the epidermal growth factor receptor (EGFR) and green fluorescent protein (GFP). A plasmid that expressed the chimeric gene and a plasmid that expressed the antisense RNA under the control of the inducible U6 promoter were used to cotransfect HeLa cells that were producing the tetracycline **repressor** protein (**Tet** R). Addn. of tetracycline to the culture medium 12 h after transfection resulted in the almost complete disappearance of the fluorescent signal due to the chimeric protein within 24 h. Our results suggest that this expression system might be a useful tool for controlling the expression of functional RNAs, such as aptamers and antisense RNAs, both in basic research and in gene therapy.

ACCESSION NUMBER: 2000:693476 CAPLUS
DOCUMENT NUMBER: 133:277165
TITLE: Recombinant human U6 snRNA gene promoter for controlling the expression of functional RNAs and therapeutic uses
INVENTOR(S): Taira, Kazumasa; Ohkawa, Atsushi; Shibata, Atsushi
PATENT ASSIGNEE(S): Agency for Industrial Science and Technology, Japan
SOURCE: Jpn. Tokkyo Koho, 18 pp.
CODEN: JTXXFF
DOCUMENT TYPE: Patent
LANGUAGE: Japanese
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
JP 3094105	B1	20001003	JP 1999-250905	19990903
JP 3094105	B2	20001003		

L28 ANSWER 9 OF 419 CAPLUS COPYRIGHT 2001 ACS

AB The present invention provides a vector comprising Translation Elongation Factor-1 .alpha. promoter and nucleic acids encoding reverse tetracycline controlled transactivator, wherein the expression of said transactivator is under the control of the EF-1.alpha. promoter. In addn., the invention provides a method of generating a reverse tetracycline controlled transactivator expression system for inducible tetracycline regulated gene expression comprising: (a) isolation of a DNA fragment encoding the reverse tetracycline controlled transactivator by restriction enzyme digestion, (b) generation of EF-1.alpha. promoter vector, by restriction enzyme digestion, (c) directional cloning of reverse tetracycline

controlled tran[redacted]tivator into EF-1.alpha. promo[redacted] vector by ligation of 5' EcoRi compati[redacted]e restriction enzyme overhangs, (d) directional cloning of reverse tetracycline controlled transactivator into EF-1.alpha. promoter vector by Klenow fragment mediated blunt end generation of 3' Bam HI end of DNA fragment encoding the reverse tetracycline controlled transactivator and 3' XbaI end of EF-1.alpha. promoter vector and (e) blunt cloning of partially ligated fragment to produce EF-1.alpha. promoter vector expressing reverse tetracycline controlled transactivator.

Thus, plasmid pEF1prtTA, contg. the rTA gene controlled by the EF-1.alpha. promoter, was prepd. This plasmid was used to control expression of transcription factor JunB and tumor suppressor Mda-7 genes in HO-1 melanoma cells.

ACCESSION NUMBER: 2000:666863 CAPLUS
DOCUMENT NUMBER: 133:248103
TITLE: Improved expression vector for consistent cellular expression of **tet** on **repressor** in multiple cell types
INVENTOR(S): Fisher, Paul B.; Gopalkrishnan, Rahul
PATENT ASSIGNEE(S): The Trustees of Columbia University in the City of New York, USA
SOURCE: PCT Int. Appl., 40 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2000055310	A1	20000921	WO 2000-US6862	20000315

W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

PRIORITY APPLN. INFO.: US 1999-268303 19990315
REFERENCE COUNT: 6
REFERENCE(S):
(1) Bujard; US 5654168 A 1997 CAPLUS
(2) Golfman; Modifications of Vectors pEF-BOS, pcDNA1 and pcDNA3 Results in Improved Convenience and Expression, BioTechniques 1996, V21(6), P1013
(3) Gossen; Transcriptional Activation by Tetracyclines in Mammalian cells, Science 1995, V268, P1766 CAPLUS
(4) Kappel; Regulating Gene Expression in Transgenic Animals, Current Opinion in Biotechnology 1992, V3, P548 CAPLUS
(5) Palmiter; Metallothionein-Human GH Fusion Genes Stimulate Growth of Mice, Science 1983, V222, P809 CAPLUS

ALL CITATIONS AVAILABLE IN THE RE FORMAT

L28 ANSWER 10 OF 419 CAPLUS COPYRIGHT 2001 ACS
AB The present invention is directed to compns. and methods for a genetic system of detecting protein-protein interactions in a mammalian host cell using a typical two-hybrid bait and test system to drive expression of one

or more reporte[redacted]enes. The individual compns. [redacted] useful for analyzing protein-protein[redacted]teractions between known prote[redacted] and to isolate, clone and characterize unknown proteins. The individual compns. can be used to express the fusion proteins either transiently or stably.

ACCESSION NUMBER: 2000:623699 CAPLUS
DOCUMENT NUMBER: 133:203833
TITLE: Two-hybrid systems for cloning genes for interacting proteins in mammalian expression hosts
INVENTOR(S): Luo, Ying; Huang, Betty; Payan, Donald
PATENT ASSIGNEE(S): Rigel Pharmaceuticals, Inc., USA
SOURCE: U.S., 18 pp.
CODEN: USXXAM
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 6114111	A	20000905	US 1998-50863	19980330

REFERENCE COUNT: 14
REFERENCE(S):
(1) Anon; WO 9731113 1997 CAPLUS
(2) Chien; Proc Natl Acad Sci USA 1991, V88, P9578 CAPLUS
(3) Dalton; US 5637463 1997 CAPLUS
(5) Erickson; US 5525490 1996 CAPLUS
(6) Fearon; Proc Natl Acad Sci USA 1992, V89, P7958 CAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

=> d 129 1-10 abs ibib

L29 ANSWER 1 OF 12 CAPLUS COPYRIGHT 2001 ACS
AB Cis-acting mutations that affect the regulation of the metB gene of S. typhimurium LT2 were isolated and characterized. The mutations were isolated in an Escherichia coli lac deletion strain lysogenized with . **lambda. bacteriophage** carrying a metB-lacZ gene fusion (.lambda.JBlac) in which .beta.-galactosidase prodn. is dependent upon metB gene expression. The mutant lysogens show **e**levated, poorly regulated .beta.-galactosidase prodn. The altered regulation is a result of disruption of the methionine control system mediated by the metJ **repressor**. The mutations are located in a region of dyad symmetry centered near the -35 sequence of the metB promoter. These mutations may alter the **repressor** binding site and define the metB operator sequence. A highly conserved, nonsym. DNA sequence of unknown function which occurs in the control regions of the metA, metC, metE, metF, metG, and metJB genes of both S. typhimurium and E. coli is discussed.

ACCESSION NUMBER: 1987:97064 CAPLUS
DOCUMENT NUMBER: 106:97064
TITLE: Mutations affecting the regulation of the metB gene of Salmonella typhimurium LT2
AUTHOR(S): Urbanowski, Mark L.; Plamann, Lynda S.; Stauffer, George V.
CORPORATE SOURCE: Dep. Microbiol., Univ. Iowa, Iowa City, IA, 52242, USA
SOURCE: J. Bacteriol. (1987), 169(1), 126-30
CODEN: JOBAAY; ISSN: 0021-9193
DOCUMENT TYPE: Journal
LANGUAGE: English

L29 ANSWER 2 OF 12 CAPLUS COPYRIGHT 2001 ACS

AB The construction of a .lambda.prm116sar2a double mutant is described. The prm mutation was characterized by the inability of the mutant bacteriophage to synthesize repressor from the promoter of maintenance of lysogeny, Prm (Gussin et al., 1975). The sar mutation, located near the origin of phage DNA replication, was shown to suppress cis-acting clear mutations (cy) for the synthesis of repressor during the establishment of lysogeny (Honigman et al., 1975). The present study shows that the inability to maintain lysogeny due to the prm- mutation is suppressed by the sar mutation. No repressor is synthesized when .lambda.prm infects immune cells whereas .lambda.prm sar2a synthesized as much as 30% of wild-type levels of repressor. The results indicate that transcription initiated near the origin of DNA replication may replace Prm for the synthesis of repressor.

ACCESSION NUMBER: 1977:185722 CAPLUS
DOCUMENT NUMBER: 86:185722
TITLE: Suppression of a Prm mutant by the sar mutation for the synthesis of repressor by bacteriophage lambda
AUTHOR(S): Oppenheim, Ariella
CORPORATE SOURCE: Hadassah Med. Sch., Hebrew Univ., Jerusalem, Israel
SOURCE: J. Mol. Biol. (1977), 111(1), 83-9
CODEN: JMOBAK
DOCUMENT TYPE: Journal
LANGUAGE: English

L29 ANSWER 3 OF 12 CAPLUS COPYRIGHT 2001 ACS
AB A review with .apprx.118 refs. describing the immunity system of the **lambda. bacteriophage** and present knowledge of the **repressor** and its action. The literature since 1971 is emphasized and in many cases the approach taken is highly speculative.

ACCESSION NUMBER: 1976:575295 CAPLUS
DOCUMENT NUMBER: 85:175295
TITLE: The .lambda. repressor and its action
AUTHOR(S): Pirrotta, Vincenzo
CORPORATE SOURCE: Abt. Mikrobiol., Univ. Basel, Basel, Switz.
SOURCE: Curr. Top. Microbiol. Immunol. (1976), 74, 21-54
CODEN: CTMIA3
DOCUMENT TYPE: Journal; General Review
LANGUAGE: English

L29 ANSWER 4 OF 12 CAPLUS COPYRIGHT 2001 ACS
AB **Lambda bacteriophage** mutants, .lambda.sar, were isolated. These mutants formed plaques on a nonlysogenic lawn and were unable to grow on nonimmune (imm-), cro constitutive hosts. Anal. of the restriction of .lambda.sar by a set of defective lysogens suggested that both the cro and cII gene products participate in the inhibition. The sar mutations were mapped in the ori region between the genes cII and O. Complementation expts. showed that under the restrictive conditions .lambda.sar was defective in the expression of both the N and O genes. Transcription analyses support these findings, as .lambda.sar was unable to serve as a template for transcription after infecting cro constitutive hosts. In addn., .lambda.sar did not replicate under restrictive conditions. The Sar phenotype was relieved by removing sites of action of cro either by a V2 mutation or by substituting the .lambda. immunity region by imm434 orimm21. Similarly introducing a cy mutation, which interferes with the action of the cII gene product, eliminated the Sar effect. The sar mutation suppressed cy mutations as manifested in plaque morphol., lysogenization frequency, cI **repressor** synthesis, and the expression of rex function. Suppression occurred only when the sar mutation was present in cis to cy and it required the action of the cII and cIII gene products. The sar mutation may suppress cy by activating a new promoter for **repressor** synthesis, pro. The cII and cIII gene products may act at a site other than y.

ACCESSION NUMBER: 1975:475276 CAPLUS
DOCUMENT NUMBER: 83:75276
TITLE: Pleiotropic regulatory mutation in .lambda. bacteriophage
AUTHOR(S): Honigman, Alik; Oppenheim, Ariella; Oppenheim, Amos B.; Stevens, Willem F.
CORPORATE SOURCE: Hadassah Med. Sch., Hebrew Univ., Jerusalem, Israel
SOURCE: Mol. Gen. Genet. (1975), 138(2), 85-111
CODEN: MGGEAE
DOCUMENT TYPE: Journal
LANGUAGE: English

L29 ANSWER 5 OF 12 CAPLUS COPYRIGHT 2001 ACS
AB A review with 27 refs. on the reiterated, nonidentical **repressor** binding sites of the .**lambda**. **bacteriophage** operators, the arrangement of these sites within each operator, and the mechanism of **repressor** action of the operator.
ACCESSION NUMBER: 1974:500785 CAPLUS
DOCUMENT NUMBER: 81:100785
TITLE: Control elements in the DNA of bacteriophage .lambda.
AUTHOR(S): Maniatis, Tom; Ptashne, Mark; Maurer, Russell
CORPORATE SOURCE: Biol. Lab., Harvard Univ., Cambridge, Mass., USA
SOURCE: Cold Spring Harbor Symp. Quant. Biol. (1974), 38, 857-68
CODEN: CSHSAZ
DOCUMENT TYPE: Journal; General Review
LANGUAGE: English

L29 ANSWER 6 OF 12 BIOSIS COPYRIGHT 2001 BIOSIS
AB An improved vector upon introduction into a suitable bacterial host containing the thermolabile **repressor** CI renders the host cell capable, upon increasing the temperature of the host cell to a temperature at which the **repressor** is destroyed, of effecting expression of a desired gene inserted into the vector and production of polypeptide encoded by the gene. The vector is a double-stranded DNA molecule which includes in 5' to 3' order the following: a DNA sequence which contains the promoter and operator PL OL from **lambda** **bacteriophage**; the N utilization site for binding antiterminator N protein produced by the host cell; a DNA sequence which contains a ribosomal binding site for rendering the mRNA of the desired gene capable of binding to ribosomes within the host cell; an ATG initiation codon or a DNA sequence which is converted into an ATG initiation codon upon insertion of the desired gene into the vector; a restriction enzyme site for inserting the desired gene into the vector in phase with the ATG initiation codon; and additionally a DNA sequence which contains an origin of replication from a bacterial plasmid capable of autonomous replication in the host cell and a DNA sequence which contains a gene associated with a selectable or identifiable trait which is manifested when the vector is present in the host cell.
ACCESSION NUMBER: 2000:466450 BIOSIS
DOCUMENT NUMBER: PREV200000466450
TITLE: Expression vectors for enhanced production of polypeptides, plasmids containing the vectors, hosts containing the plasmids, products manufactured thereby and related methods.
AUTHOR(S): Gorecki, Marian (1); Levanon, Avigdor; Oppenheim, Amos; Vogel, Tikva
CORPORATE SOURCE: (1) Rehovot Israel
ASSIGNEE: Bio-Technology General Corp.
PATENT INFORMATION: US 6054291 April 25, 2000
SOURCE: Official Gazette of the United States Patent and Trademark

ice Patents, (Apr. 25, 2000) V 1233, No. 4, pp. No
ination. e-file.
ISSN: 0098-1133.

DOCUMENT TYPE: Patent
LANGUAGE: English

L29 ANSWER 7 OF 12 BIOSIS COPYRIGHT 2001 BIOSIS
AB We isolated and characterized cis-acting mutations that affect the regulation of the metB gene of Salmonella typhimurium LT2. The mutations were isolated in an Escherichia coli lac deletion strain lysogenized with **.lambda. bacteriophage** carrying a metB-lacZ gene fusion (.lambda.JBlac) in which .beta.-galactosidase production is dependent upon metB gene expression. The mutant lysogens show elevated, poorly regulated .beta.-galactosidase production. The altered regulation is a result of disruption of the methionine control system mediated by the metJ **repressor**. The mutations are located in a region of dyad symmetry centered near the -35 seguence of the metB promoter. We propose that these mutations alter the **repressor** binding site and define the metB operator seguence. In addition, we discuss a highly conserved, nonsymmetric DNA sequence of unknown function which occurs in the control regions of the metA, metC, metE, metF, metG, and metJB genes of both S. typhimurium and E. coli.
ACCESSION NUMBER: 1987:125486 BIOSIS
DOCUMENT NUMBER: BA83:64547
TITLE: MUTATIONS AFFECTING THE REGULATION OF THE MET-B GENE OF SALMONELLA-TYPHIMURIUM LT2.
AUTHOR(S): URBANOWSKI M L; PLAMANN L S; STAUFFER G V
CORPORATE SOURCE: DEP. MICROBIOL., UNIV. IOWA, IOWA CITY, IOWA 52242, USA.
SOURCE: J BACTERIOL, (1987) 169 (1), 126-130.
CODEN: JOBAAY. ISSN: 0021-9193.
FILE SEGMENT: BA; OLD
LANGUAGE: English

L29 ANSWER 8 OF 12 BIOSIS COPYRIGHT 2001 BIOSIS
AB Superinfection of Corynebacterium diphtheriae C7(.beta.) by heteroimmune phage .gamma. is productive, whereas superinfection by .gamma.-bin mutants is for the most part nonproductive. Exclusion of .gamma.-bin phage occurred after its DNA penetrated and was partially expressed in the heteroimmune lysogen. All of the infected cells were killed, and lysis was observed. The .beta. inhibitor causing exclusion was produced during the prophage state and appeared to be distinct from immune **repressor**. The ability of .gamma.-bin phage to superinfect C7(.beta.) productively could be restored by recombination with .beta. phage, indicating that both .beta. and .gamma. phages contain either identical or similar alleles of the bin gene. The bin gene was mapped by vegetative and prophage crosses and found to be located in the region of the phage genome concerned with regulation. Both .beta. and .gamma. wild-type phages induced the resident prophage in a significant fraction of superinfected heteroimmune lysogens. This, coupled with the fact that induction of C7(.beta.) abolished exclusion, suggests that the bin gene product acts as antirepressor; i.e., it reduces the level of heteroimmune **repressor** either directly or indirectly. The .gamma.-bin mutants either failed to produce antirepressor or did so with reduced efficiency. Antirepressor activity was negatively controlled by homoimmune **repressor**. The isolation of .beta. mutants that appeared bin-like suggests that .beta. and .gamma. phages contain homologous systems of exclusion and antiexclusion. Exclusion of .gamma.-bin by .beta. phage in gram-positive C. diphtheriae exhibited striking parallels to the sieB exclusion described for phages P22 and .lambda. in gram-negative organisms. The extended similarities of these corynephages to **.lambda. bacteriophage** is noted.

ACCESSION NUMBER: [redacted]1:182218 BIOSIS
DOCUMENT NUMBER: [redacted]1:52210
TITLE: SUPER INFECTION EXCLUSION BY HETERO IMMUNE CORYNEBACTERIO PHAGES.
AUTHOR(S): GROMAN N B; RABIN M
CORPORATE SOURCE: DEP. OF MICROBIOL. AND IMMUNOL., SCH. OF MED., UNIV. OF WASHINGTON, SEATTLE, WASH. 98195.
SOURCE: J VIROL, (1980) 36 (2), 526-532.
CODEN: JOVIAM. ISSN: 0022-538X.
FILE SEGMENT: BA; OLD
LANGUAGE: English

L29 ANSWER 9 OF 12 BIOSIS COPYRIGHT 2001 BIOSIS
AB In the lac operon, the existence of a secondary **repressor** binding site, inside the Z gene, was inferred from in vitro binding studies. A series of deletions was constructed from a lac transducing . **lambda. bacteriophage**. Some of those deleted bacteriophages still have the property of derepressing a chromosomal lac operon, even though they no longer contain the lac operator. This phenomenon is an indication that the secondary **repressor** binding site is also active in vivo.
ACCESSION NUMBER: 1979:180134 BIOSIS
DOCUMENT NUMBER: BA67:60134
TITLE: BINDING OF LAC REPRESSOR TO THE SECONDARY LAC OPERATOR IN ESCHERICHIA-COLI.
AUTHOR(S): RAMBACH A; LEBASTARD M
CORPORATE SOURCE: INST. PASTEUR, 28 RUE DU DR. ROUX, PARIS 15E, FR.
SOURCE: MOL GEN GENET, (1978) 166 (2), 229-231.
CODEN: MGGEAE. ISSN: 0026-8925.
FILE SEGMENT: BA; OLD
LANGUAGE: English

L29 ANSWER 10 OF 12 CEABA-VTB COPYRIGHT 2001 DECHEMA
AN 1998(07):0391 CEABA-VTB FS B
AB A plasmid for producing SOD or its analogue is disclosed which, upon introduction into a suitable bacterial host containing the thermolabile **repressor** CI, renders the host cell capable, upon increasing the temperature of the host cell to a temperature at which the **repressor** is destroyed, of effecting expression of DNA encoding SOD to produce the enzyme. The plasmid is a ds DNA molecule which includes in 5 to 3 order: a DNA sequence containing the promoter and operator PLOL from.**lambda. bacteriophage**; the N utilization site for binding antiterminator N protein produced by the host cell; a DNA sequence that contains a ribosomal binding site for rendering the mRNA of the gene encoding SOD capable of binding to ribosomes within the host cell; and an ATG initiation codon. the plasmid further includes: a restriction enzyme site for inserting the gene encoding SOD; and another DNA sequence containing an origin of replication from a bacterial plasmid capable of autonomous replication in the host cell and a DNA sequence containing a gene associated with an identifiable or selectable trait which is apparent when the plasmid is present in the host cell.
FILE SEGMENT B
DOCUMENT NUMBER: CEABA: 1998:5484891
TITLE: Bacterial expression of superoxide dismutase (SOD)
AUTHOR: Aviv, H.; Gorecki, M.; Levanon, A.; Oppenheim, A.; Hartman, J. (Bio-Technol. General Corp., Iselin, NJ, USA)
SOURCE: US Patent (1997) US 5670371(Appl. EP 84107717 Filed 3 Jul 1984)
CODEN: USXXAM
DOCUMENT TYPE: Patent
LANGUAGE: English

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